



Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

SEQ ID NO: 5  
(nr)

The request ID is 1060818008-0485-22286

**Format!** or **Reset all**

The results are estimated to be ready in 33 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Hit Table

Start formatting  
from query #

Limit results by  
entrez query or select from: (none)

Expect value  
range:

Results file ☐



Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

SEE ID NO: 6  
(NR)

The request ID is 1060818067-0938-25515

**Format!** or **Reset all**

The results are estimated to be ready in 28 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment  in

Number of: Descriptions   Alignments

Alignment view

Start formatting from query #

Limit results by  or select from:

Expect value range:

Results file ☐

 **NCBI**  
Nucleotide      Protein      Translations      Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

SEQ ID NO: 7  
(nr)

The request ID is 1060818116-8188-1510948.BLASTQ4

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment  in  HTML

Number of: Descriptions  100  Alignments  50

Alignment view  Hit Table

Start formatting  
from query #

Limit results by  or select from:  (none)

Expect value  
range:

Results file ☐

 **NCBI**  
Nucleotide      Protein      Translations      Retrieve results for an RID

*formatting* **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (3283 letters)

SEQ ID NO: 8  
(nr)

The request ID is 1060818177-8586-2227958.BLASTQ4

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Hit Table

Start formatting  
from query #

Limit results by  
entrez query or select from: (none)

Expect value  
range:

Results file ☐





# results of BLAST

TBLASTX 2.2.6 [Apr-09-2003]

RID: 1061911388-17096-1581453.BLASTQ3

Query=

(1708 letters)

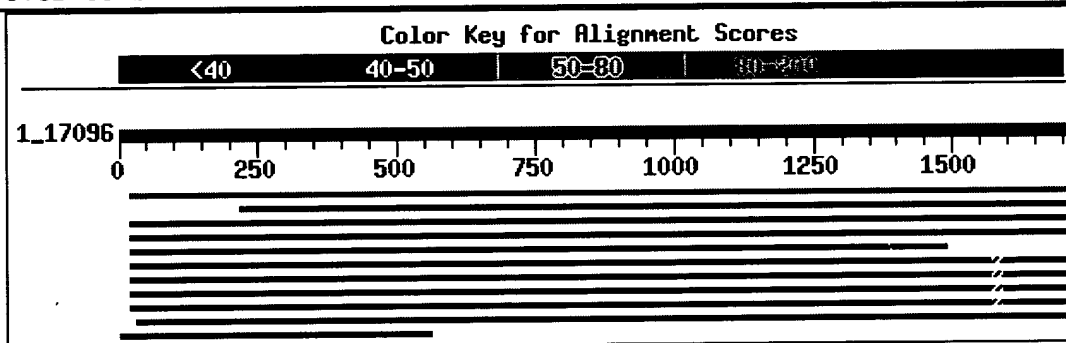
*translated  
seq 5*

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,886,208 sequences; 8,918,056,233 total letters

Taxonomy reports

## Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value N

gi 4191607 gb AF117106.1 AF117106	Homo sapiens IGF-II m...	709	0.0	6	LUG
gi 21361351 ref NM_006546.2	Homo sapiens IGF-II mRNA-b...	576	0.0	6	LUG
gi 7141071 gb AF198254.1 AF198254	Homo sapiens mRNA-bin...	576	0.0	6	LUG
gi 24580458 gb AC105030.11	Homo sapiens chromosome 17,...	363	0.0	12	
gi 22760672 dbj AK074915.1	Homo sapiens cDNA FLJ90434 ...	709	0.0	4	UG
gi 3273748 gb AF061569.1 AF061569	Mus musculus coding r...	525	0.0	9	LUG
gi 31560605 ref NM_009951.2	Mus musculus insulin-like ...	525	0.0	9	LG
gi 12851513 dbj AK013940.1	Mus musculus 13 days embryo...	525	0.0	9	LUG
gi 26336870 dbj AK044850.1	Mus musculus 9.5 days embryo...	525	0.0	9	LU
gi 30354043 gb BC051679.1	Mus musculus insulin-like gr...	522	0.0	9	L
gi 31342209 ref NM_175594.2	Rattus norvegicus IGF-II m...	529	0.0	7	L
gi 27464837 gb AF541940.1	Rattus norvegicus b-actin zi...	529	0.0	7	L
gi 2570920 gb AF026527.1 AF026527	Gallus gallus zipcode...	504	0.0	6	
gi 27689046 ref XM_220886.1	Rattus norvegicus similar ...	529	0.0	6	L
gi 22204252 emb AL606704.20	Mouse DNA sequence from cl...	218	0.0	15	
gi 21954991 gb AC098642.5	Genomic sequence for Mus mus...	218	0.0	14	

gi 14475918 gb AC084407.10	Mus Musculus Strain C57BL6/...	218	0.0	14	
gi 3172448 gb AF064634.1 AF064634	Xenopus laevis Vg1 RN...	341	0.0	5	
gi 3136157 gb AF055923.1 AF055923	Xenopus laevis RNA bi...	341	0.0	5	
gi 2801765 gb AF042353.1 AF042353	Xenopus laevis KH dom...	341	0.0	5	
gi 3172446 gb AF064633.1 AF064633	Xenopus laevis Vg1 RN...	341	0.0	5	
gi 28278435 gb BC045873.1	Danio rerio decapentaplegic ...	336	0.0	5	L
gi 18858570 ref NM 131491.1	Danio rerio decapentaplegi...	336	0.0	5	L
gi 5596631 gb AF161270.1 AF161270	Danio rerio Vg1 RNA b...	336	0.0	5	L
gi 30795211 ref NM 006547.2	Homo sapiens IGF-II mRNA-b...	374	0.0	5	L G
gi 4191611 gb AF117108.1 AF117108	Homo sapiens IGF-II m...	374	0.0	5	L G
gi 29145080 gb BC049082.1	Mus musculus insulin-like gr...	377	0.0	5	L
gi 12847972 dbj AK011689.1	Mus musculus 10 days embryo...	377	0.0	5	L G
gi 28175448 gb BC045138.1	Mus musculus insulin-like gr...	377	0.0	5	L
gi 11933383 dbj AB046173.1	Mus musculus mimp3 mRNA for...	377	0.0	5	L G
gi 2105468 gb U97188.1 HSU97188	Homo sapiens putative R...	374	0.0	5	L G
gi 4098296 gb U76705.1 HSU76705	Human putative RNA bind...	374	0.0	5	L G
gi 31542991 ref NM 023670.2	Mus musculus insulin-like ...	377	0.0	5	L G
gi 26353479 dbj AK088465.1	Mus musculus 2 days neonate...	377	0.0	5	L
gi 27552765 ref NM 006548.2	Homo sapiens IGF-II mRNA-b...	327	0.0	5	L
gi 33878041 gb BC021290.2	Homo sapiens IGF-II mRNA-bin...	327	0.0	5	L
gi 4191609 gb AF117107.1 AF117107	Homo sapiens IGF-II m...	327	0.0	5	L
gi 26093366 dbj AK049196.1	Mus musculus ES cells cDNA,...	324	0.0	6	L
gi 23958572 gb BC023758.1	Mus musculus RIKEN cDNA C330...	324	0.0	6	L
gi 26090647 dbj AK044984.1	Mus musculus 9.5 days embryo...	324	0.0	6	L
gi 4883680 gb AF057352.1 AF057352	Homo sapiens hepatoce...	327	0.0	4	
gi 26097330 dbj AK077404.1	Mus musculus 6 days neonate...	324	e-179	7	L
gi 27666189 ref XM 221343.1	Rattus norvegicus similar ...	315	e-175	5	L
gi 33942111 ref NM 183029.1	Mus musculus RIKEN cDNA C3...	313	e-173	5	L
gi 32451876 gb BC054552.1	Mus musculus cDNA clone MGC:...	313	e-173	5	L
gi 7656675 gb AC020629.6	Homo sapiens 12q BAC RP11-76E...	235	e-161	6	
gi 3646096 emb AL023775.1 HS497J21	Human DNA sequence f...	308	e-152	6	
gi 15552942 emb AL596177.4	Human DNA sequence from clo...	285	e-142	5	
gi 19849375 gb AC104980.5	Homo sapiens chromosome 8, c...	259	e-133	5	
gi 17298202 dbj AP004290.2	Homo sapiens genomic DNA, c...	259	e-133	5	
gi 27413166 gb AC016961.28	Homo sapiens 3 BAC RP11-394...	100	e-126	10	
gi 33284913 emb BX088533.9	Zebrafish DNA sequence from...	95	e-120	9	
gi 26081662 dbj AK030096.1	Mus musculus adult male tes...	205	e-111	4	
gi 27710325 ref XM 231739.1	Rattus norvegicus similar ...	376	e-101	2	L
gi 30148117 ref XM 291469.2	Homo sapiens similar to he...	264	3e-94	3	L
gi 18873962 gb AC092447.5	Homo sapiens BAC clone RP11-...	250	3e-89	4	L
gi 30520355 ref NG 002770.1	Homo sapiens pseudogene of...	250	3e-89	4	L
gi 30151067 ref XM 302320.1	Homo sapiens similar to IG...	242	4e-87	4	L
gi 31240026 ref XM 320427.1	Anopheles gambiae ENSANGP0...	122	4e-86	5	
gi 28492961 ref XM 193835.2	Mus musculus RIKEN cDNA C3...	323	1e-85	3	L
gi 21637524 gb AC091133.11	Homo sapiens chromosome 17,...	232	3e-85	5	
gi 28571360 ref NM 167254.2	Drosophila melanogaster IG...	124	3e-84	5	L
gi 17862977 gb AY069821.1	Drosophila melanogaster SD07...	124	3e-84	5	L
gi 7533028 gb AF241237.1 AF241237	Drosophila melanogast...	124	4e-84	5	L
gi 24641109 ref NM 167255.1	Drosophila melanogaster IG...	124	5e-84	5	
gi 28571361 ref NM 078556.3	Drosophila melanogaster IG...	124	5e-84	5	

gi 24641096 ref NM_167249.1	Drosophila melanogaster IG...	124	6e-84	5
gi 24641098 ref NM_167250.1	Drosophila melanogaster IG...	124	7e-84	5
gi 24641104 ref NM_167253.1	Drosophila melanogaster IG...	124	9e-84	5
gi 24641102 ref NM_167252.1	Drosophila melanogaster IG...	124	9e-84	5
gi 24641100 ref NM_167251.1	Drosophila melanogaster IG...	124	9e-84	5
gi 25012806 gb BT001739.1	Drosophila melanogaster RE72...	124	2e-83	5
gi 30581644 gb AC094527.7	Rattus norvegicus 5 BAC CH23...	122	3e-80	9
gi 13446341 gb AC021876.5	Homo sapiens BAC clone GS1-1...	121	9e-80	5
gi 27485839 ref XM_208686.1	Homo sapiens similar to he...	192	8e-77	3
gi 532210 gb L35549.1 MUSYBIC	Mus musculus Y-box bindin...	169	2e-72	5
gi 13446351 gb AC005082.3	Homo sapiens BAC clone CTA-2...	94	2e-54	5
gi 27710263 ref XM_216143.1	Rattus norvegicus similar ...	205	4e-50	2
gi 25100579 gb AC125292.4	Drosophila melanogaster X BA...	125	3e-39	4
gi 22832049 gb AE003484.2	Drosophila melanogaster chro...	125	9e-38	4
gi 28514171 ref XM_286404.1	Mus musculus hypothetical ...	74	4e-31	5
gi 26102680 dbj AK085396.1	Mus musculus 0 day neonate ...	69	1e-29	5
gi 33086575 gb AY325199.1	Rattus norvegicus Ab2-255 mR...	119	7e-27	2
gi 26090795 dbj AK045244.1	Mus musculus 9.5 days embry...	124	8e-26	1
gi 27709099 ref XM_228991.1	Rattus norvegicus similar ...	100	2e-18	1
gi 17554287 ref NM_065522.1	Caenorhabditis elegans put...	51	5e-15	3
gi 508101 emb Z34802.1 CEM88	Caenorhabditis elegans cos...	51	2e-12	3
gi 32423212 ref XM_332043.1	Neurospora crassa strain O...	56	7e-12	2
gi 26330215 dbj AK034811.1	Mus musculus 12 days embryo...	51	6e-11	4
gi 10947013 ref NM_021568.1	Mus musculus poly(rC) bind...	51	6e-11	4
gi 9957160 gb AF176327.1 AF176327	Mus musculus alphaCP-...	51	6e-11	4
gi 27503478 gb BC042440.1	Mus musculus poly(rC) bindin...	51	6e-11	4
gi 2644965 emb AJ003023.1 OCHNRNPE1	Oryctolagus cunicul...	49	1e-10	4
gi 14141164 ref NM_006196.2	Homo sapiens poly(rC) bind...	49	2e-10	4
gi 24980782 gb BC039742.1	Homo sapiens, clone MGC:4756...	49	2e-10	4
gi 444020 emb Z29505.1 HSNUACBIP	H.sapiens mRNA for nuc...	49	2e-10	4
gi 460770 emb X78137.1 HSRNPE1	H.sapiens hnRNP-E1 mRNA	49	2e-10	4
gi 1215670 gb U24223.1 HSU24223	Human alpha-CP1 mRNA, c...	49	2e-10	4
gi 26348075 dbj AK079564.1	Mus musculus adult male hyp...	51	3e-10	3
gi 21753334 dbj AK094301.1	Homo sapiens cDNA FLJ36982 ...	51	3e-10	3

## Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein  
Length = 2130

Score = 709 bits (1543), Expect(4) = 0.0  
Identities = 306/335 (91%), Positives = 308/335 (91%)  
Frame = +2 / +1

Query: 704 AMSSHLIPGLNLAAGVGLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883  
++ SHLIPGLNLAAGVGLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG  
Sbjct: 1084 SLQSHLIPGLNLAAGVGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1263

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1063  
AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN  
Sbjct: 1264 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1443

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243  
 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK  
 Sbjct: 1444 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1623

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRKXXXXXXXXXESRTTGRNRECA 1423  
 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK ESRTTGRNRECA  
 Sbjct: 1624 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK\*PAPPCPFESRTTGRNRECA 1803

Query: 1424 LPGRPENEWESGTGPGCRSGLPT\*LRKMFQ\*GTLIQPTPTQLAQHCXPLGVSEIXAQ 1603  
 LPGRPENEWESGT GPGCRSGLPT\*LRKMFQ\*GTLI QPQTPTQLAQHC PLGVSEI AQ  
 Sbjct: 1804 LPGRPENEWESGTPGPGCRSGLPT\*LRKMFQ\*GTLISQPQTPTQLAQHCLPLGVSEILAQ 1983

Query: 1604 GTFKRGLFKEALQAPPRGWITPQWEEK\*NFLQVLK 1708  
 GTFKRGLFKEALQAPPRGWITPQWEEK\*NFLQVLK  
 Sbjct: 1984 GTFKRGLFKEALQAPPRGWITPQWEEK\*NFLQVLK 2088

Score = 644 bits (1400), Expect(5) = 0.0  
 Identities = 265/290 (91%), Positives = 265/290 (91%)  
 Frame = +3 / +2

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXXPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016  
 PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP  
 Sbjct: 1217 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1396

Query: 1017 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1196  
 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\*  
 Sbjct: 1397 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1576

Query: 1197 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1376  
 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP  
 Sbjct: 1577 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1756

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD\*ERCXXXXXXXXXXKHPPN 1556  
 VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD\*ERC KHPPN  
 Sbjct: 1757 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD\*ERCSEEP\*SLSPKHPPN 1936

Query: 1557 WPNTVCPSGCQKX\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF\* 1706  
 WPNTVCPSGCQK \*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF\*  
 Sbjct: 1937 WPNTVCPSGCQKF\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF\* 2086

Score = 634 bits (1378), Expect(4) = 0.0  
 Identities = 267/283 (94%), Positives = 267/283 (94%)  
 Frame = -3 / -3

Query: 1706 LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALXFLTPRGAXSVGPIGWVFGAXRS 1527  
 LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLAL FLTPRGA SVGPIGWVFGA RS  
 Sbjct: 2086 LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALEFLTPRGADSVGPIGWVFGAERS 1907

Query: 1526 GFLTGTFSFIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTXRDREGLVTXXXX 1347  
 GFLTGTFSFIKWANLIYSPA VSRIPTHSQACRGEHTLDFCPLLSWT RDREGLVT  
 Sbjct: 1906 GFLTGTFSFIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTRRDREGLVTSSVP 1727

Query: 1346 XXXXXXSDAAA\*PGPGCLGSSVEPSDWHNR\*FSR\*PGRSHQGSGLLVLPQLPSNSA 1167  
SDAAA\*PGPGCLGSSVEPSDWHNR\*FSR\*PGRSHQGSGLLVLPQLPSNSA  
Sbjct: 1726 GPGYSVPSDAAA\*PGPGCLGSSVEPSDWHNR\*FSR\*PGRSHQGSGLLVLPQLPSNSA 1547

Query: 1166 TRSPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRRFFPEP\*IGPLAVQ\*\*\*P 987  
TRSPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRRFFPEP\*IGPLAVQ\*\*\*P  
Sbjct: 1546 TRSPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRRFFPEP\*IGPLAVQ\*\*\*P 1367

Query: 986 YELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T 858  
YELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T  
Sbjct: 1366 YELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T 1238

Score = 557 bits (1211), Expect(3) = 0.0  
Identities = 228/237 (96%), Positives = 233/237 (98%)  
Frame = -1 / -1

Query: 739 QVQARDQVRAHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 560  
Q + + +++AHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF  
Sbjct: 1113 QARDQVRLQAHGSIIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 934

Query: 559 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 380  
CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG  
Sbjct: 933 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 754

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG 200  
GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG  
Sbjct: 753 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLLG 574

Query: 199 WGP RCHR\*ALAGLT PRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDGSPG 29  
WGP RCHR\*ALAGLT PRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDG PG  
Sbjct: 573 WGP RCHR\*ALAGLT PRAKAPSAPILRSLCYLLIGDVGD LQGMVLQLVAIQLHDGLPG 403

Score = 529 bits (1150), Expect(3) = 0.0  
Identities = 226/227 (99%), Positives = 226/227 (99%)  
Frame = +2 / +1

Query: 32 RGAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPVAAGAPAKQQ 211  
R AIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPVAAGAPAKQQ  
Sbjct: 406 RGAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPVAAGAPAKQQ 585

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391  
QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG  
Sbjct: 586 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 765

Query: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571  
CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI  
Sbjct: 766 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 945

Query: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712  
SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS  
Sbjct: 946 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1086

Score = 512 bits (1113), Expect(3) = 0.0  
Identities = 204/208 (98%), Positives = 204/208 (98%)  
Frame = -2 / -2

Query: 1707 FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG\*XI 1528  
FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG\* I  
Sbjct: 2087 FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG\*EI 1908

Query: 1527 RVPHWNIFLNQVGKPDLPQGPXVPDSSHFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA 1348  
RVPHWNIFLNQVGKPDLPQGP VPDSSHFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA  
Sbjct: 1907 RVPHWNIFLNQVGKPDLPQGPVDPDSSHFSGLPGRAHSRFLPVVVLDSKGQGGAGHFLRA 1728

Query: 1347 WAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC 1168  
WAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC  
Sbjct: 1727 WAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAAVKFC 1548

Query: 1167 NSFTVPPLPMTRPAADAGTRMWSSFT 1084  
NSFTVPPLPMTRPAADAGTRMWSSFT  
Sbjct: 1547 NSFTVPPLPMTRPAADAGTRMWSSFT 1464

Score = 504 bits (1094), Expect(3) = 0.0  
Identities = 194/194 (100%), Positives = 194/194 (100%)  
Frame = +1 / +3

Query: 715 SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHRH 894  
SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHRH  
Sbjct: 1095 SPDPWPEPGCCRSFSPFIQRSPAASQORYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHRH 1274

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1074  
QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS  
Sbjct: 1275 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1454

Query: 1075 QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT 1254  
QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT  
Sbjct: 1455 QGGSEAGDPHTCASISSWPGHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT 1634

Query: 1255 FLCQSDGSTEDPRH 1296  
FLCQSDGSTEDPRH  
Sbjct: 1635 FLCQSDGSTEDPRH 1676

Score = 485 bits (1054), Expect(6) = 0.0  
Identities = 197/213 (92%), Positives = 197/213 (92%)  
Frame = -1 / -1

Query: 1513 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334  
EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLPPC  
Sbjct: 1893 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPPCLGLVT 1714

Query: 1333 XXXXXXXXXXXLQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR 1154  
LQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR  
Sbjct: 1713 LSLMLLLNLQGDVSDLP LSHLTGIEMSDDFHD DLVVLIRGLVSWYYHLSCRQILQLVHR 1534

Query: 1153 FSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974  
 FSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG  
 Sbjct: 1533 FSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1354

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875  
 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC  
 Sbjct: 1353 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1255

Score = 396 bits (858), Expect(4) = 0.0  
 Identities = 169/179 (94%), Positives = 169/179 (94%)  
 Frame = -2 / -2

Query: 711 LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 532  
 LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF  
 Sbjct: 1085 LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 906

Query: 531 RFRPSLPMRPTKLLWARIFRGTXXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352  
 RFRPSLPMRPTKLLWARIFRGTX LCIISKIILQAEQPSGVECTLMAFSA  
 Sbjct: 905 RFRPSLPMRPTKLLWARIFRGTXSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 726

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRGMSTCCCLAGAPAAATGE 175  
 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRGMSTCCCLAGAPAAATGE  
 Sbjct: 725 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRGMSTCCCLAGAPAAATGE 549

Score = 269 bits (582), Expect(6) = 0.0  
 Identities = 113/134 (84%), Positives = 113/134 (84%)  
 Frame = -3 / -3

Query: 701 PHHSHRPPELSSLFPARPCNNSRXXXXXXXXXXQGCKG\*GLATTRW\*FLSRYLALPSSGSV 522  
 PHHSHRPPELSSLFPARPCNNSR QGCKG\*GLATTRW\*FLSRYLALPSSGSV  
 Sbjct: 1075 PHHSHRPPELSSLFPARPCNNSRWPPSQ\*WSSQGCKG\*GLATTRW\*FLSRYLALPSSGSV 896

Query: 521 LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYAXXXXXXXXXXXXXPQGWSAH\*WLFQLHLR 342  
 LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYA PQGWSAH\*WLFQLHLR  
 Sbjct: 895 LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYA\*SPRSSYKRRSSPQGWSAH\*WLFQLHLR 716

Query: 341 SPSYARLSWTGSVL 300  
 SPSYARLSWTGSVL  
 Sbjct: 715 SPSYARLSWTGSVL 674

Score = 258 bits (557), Expect(3) = 0.0  
 Identities = 109/112 (97%), Positives = 109/112 (97%)  
 Frame = +1 / +3

Query: 1372 SLXLVQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH 1551  
 SLXLVQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH  
 Sbjct: 1752 SLXLVQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH 1931

Query: 1552 PIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK 1707  
 PIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK  
 Sbjct: 1932 PIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK 2087

Score = 248 bits (535), Expect(3) = 0.0  
Identities = 102/103 (99%), Positives = 103/103 (100%)  
Frame = -2 / -2

Query: 1020 NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841  
NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC  
Sbjct: 1400 NWASGGPVMITIRTLESGVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1221

Query: 840 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*E 712  
SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*+  
Sbjct: 1220 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*D 1092

Score = 230 bits (496), Expect(4) = 0.0  
Identities = 99/99 (100%), Positives = 99/99 (100%)  
Frame = +3 / +2

Query: 414 SWRLCIKRLRTPKRLTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 593  
SWRLCIKRLRTPKRLTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP  
Sbjct: 788 SWRLCIKRLRTPKRLTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 967

Query: 594 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFG RPMRMMWLP\* 710  
FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFG RPMRMMWLP\*  
Sbjct: 968 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFG RPMRMMWLP\* 1084

Score = 223 bits (482), Expect(5) = 0.0  
Identities = 88/88 (100%), Positives = 88/88 (100%)  
Frame = +3 / +2

Query: 114 HRDLRMGAEGALALGVSPARAHLWQRGQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA 293  
HRDLRMGAEGALALGVSPARAHLWQRGQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA  
Sbjct: 488 HRDLRMGAEGALALGVSPARAHLWQRGQPSSSKWTSPPFGSWCPPSMWVPLLARRGPPSA 667

Query: 294 TSQNRPSPR\*TCIGRRTQVQLKKPSVCT 377  
TSQNRPSPR\*TCIGRRTQVQLKKPSVCT  
Sbjct: 668 TSQNRPSPR\*TCIGRRTQVQLKKPSVCT 751

Score = 196 bits (422), Expect(5) = 0.0  
Identities = 78/78 (100%), Positives = 78/78 (100%)  
Frame = +1 / +3

Query: 424 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603  
YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP  
Sbjct: 798 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 977

Query: 604 \*EDHHCEGGHRELLQGRA 657  
\*EDHHCEGGHRELLQGRA  
Sbjct: 978 \*EDHHCEGGHRELLQGRA 1031

Score = 132 bits (282), Expect(4) = 0.0  
Identities = 50/55 (90%), Positives = 50/55 (90%)  
Frame = +1 / +3



Query: 19 PQFTPGSHHEAEWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 183  
P SHHEAEWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC  
Sbjct: 393 PGADQASHHEAEWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 557

Score = 125 bits (268), Expect(4) = 0.0  
Identities = 45/45 (100%), Positives = 45/45 (100%)  
Frame = +1 / +3

Query: 250 VCGCHYWQGGGHHHPQHHTDPVQDRRA\*EGERRCS\*KSHQCALHP 384  
VCGCHYWQGGGHHHPQHHTDPVQDRRA\*EGERRCS\*KSHQCALHP  
Sbjct: 624 VCGCHYWQGGGHHHPQHHTDPVQDRRA\*EGERRCS\*KSHQCALHP 758

Score = 115 bits (245), Expect(6) = 0.0  
Identities = 46/48 (95%), Positives = 46/48 (95%)  
Frame = -1 / -1

Query: 1708 F\*NLKEILFFFPLRCDPPSWWGLESTFKSALRXNF\*HPEGXTV 1565  
F\*NLKEILFFFPLRCDPPSWWGLESTFKSALR NF\*HPEG TV  
Sbjct: 2088 F\*NLKEILFFFPLRCDPPSWWGLESTFKSALR\*NF\*HPEGQTV 1945

Score = 86.3 bits (182), Expect(4) = 0.0  
Identities = 36/36 (100%), Positives = 36/36 (100%)  
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 713  
AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR  
Sbjct: 1200 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 1093

Score = 85.4 bits (180), Expect(4) = 0.0  
Identities = 31/31 (100%), Positives = 31/31 (100%)  
Frame = -2 / -2

Query: 129 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 37  
FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA  
Sbjct: 503 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 411

Score = 81.2 bits (171), Expect(6) = 0.0  
Identities = 35/49 (71%), Positives = 35/49 (71%)  
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX\*WL 36  
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR \*WL  
Sbjct: 556 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS\*WL 410

Score = 56.5 bits (117), Expect(6) = 0.0  
Identities = 21/21 (100%), Positives = 21/21 (100%)  
Frame = -3 / -3

Query: 809 QPQ\*RCWEAAGLRWMKLGKDL 747  
QPQ\*RCWEAAGLRWMKLGKDL  
Sbjct: 1189 QPQ\*RCWEAAGLRWMKLGKDL 1127

Score = 42.8 bits (87), Expect(2) = 2e-06  
Identities = 13/37 (35%), Positives = 26/37 (70%)  
Frame = +2 / +1

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 328  
++PL++L +VG +IGKEG ++ + + T++KI +  
Sbjct: 835 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 945

Score = 42.8 bits (87), Expect(2) = 2e-06  
Identities = 13/37 (35%), Positives = 26/37 (70%)  
Frame = +2 / +1

Query: 461 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571  
++PL++L +VG +IGKEG ++ + + T++KI +  
Sbjct: 592 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 702

Score = 40.9 bits (83), Expect(2) = 2e-06  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +1

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1489 VPASAAGRVIIGKGGKTVNELQNLTAEEVVPRDQTPDENDQVIV 1620

Score = 40.9 bits (83), Expect(2) = 2e-06  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +1

Query: 1109 VPASAAGRVIIGKGGKTVNELQNLTAEEVVPRDQTPDENDQVIV 1240  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1243 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1374

Score = 38.6 bits (78), Expect = 6.8  
Identities = 15/54 (27%), Positives = 30/54 (55%)  
Frame = +2 / +1

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388  
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
Sbjct: 1231 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1392

Score = 38.6 bits (78), Expect = 6.8  
Identities = 15/54 (27%), Positives = 30/54 (55%)  
Frame = +2 / +1

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012  
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
Sbjct: 601 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 762

Score = 35.4 bits (71), Expect(6) = 0.0  
Identities = 11/11 (100%), Positives = 11/11 (100%)  
Frame = -3 / -3

Query: 260 HPHTGWAPGAE 228  
HPHTGWAPGAE  
Sbjct: 634 HPHTGWAPGAE 602

Score = 30.4 bits (60), Expect(5) = 0.0  
Identities = 12/13 (92%), Positives = 13/13 (100%)  
Frame = +3 / +2

Query: 30 PGEPS\*S\*MATSW 68  
PG+PS\*S\*MATSW  
Sbjct: 404 PGKPS\*S\*MATSW 442

Score = 26.7 bits (52), Expect(5) = 0.0  
Identities = 11/11 (100%), Positives = 11/11 (100%)  
Frame = +3 / +2

Query: 747 \*VFSQLHPAQS 779  
\*VFSQLHPAQS  
Sbjct: 1127 \*VFSQLHPAQS 1159

>gi|21361351|ref|NM\_006546.2| Homo sapiens IGF-II mRNA-binding protein 1 (IM)  
Length = 2381

Score = 576 bits (1252), Expect(3) = 0.0  
Identities = 251/279 (89%), Positives = 253/279 (90%)  
Frame = +2 / +3

Query: 704 AMSSHLIPGLNLAAGVLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883  
++ SHL PGLNLAAGVLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG  
Sbjct: 1380 SLQSHLTPGLNLAAGVLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1559

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1063  
AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN  
Sbjct: 1560 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1739

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243  
FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK  
Sbjct: 1740 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1919

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRKXXXXXXXXXESRTTGRNRECA 1423  
IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK ESRTTGRNRECA  
Sbjct: 1920 IIGHFYASQMAQRKIRDILAQVKQHQKQSNQAQARRK\*PAPPCPFESRTTGRNRECA 2099

Query: 1424 LPGRPENEWESGTGPGCRSGLPT\*LRKMFQ\*GTLIXQP 1540  
LPGRPENEWESGT GPGCRSGLPT\*LRKMFQ\*GTLI QP  
Sbjct: 2100 LPGRPENEWESGTPGPGCRSGLPT\*LRKMFQ\*GTLISQP 2216

Score = 555 bits (1206), Expect(4) = 0.0  
Identities = 227/237 (95%), Positives = 232/237 (97%)  
Frame = -1 / -1

Query: 739 QVQARDQVRAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 560  
Q + + +AHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF  
Sbjct: 1409 QARGQVRLQAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 1230

Query: 559 CLGILLYLLQVPSFLANETPYKVMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 380  
CLGILLYLLQVPSFLANETPYKVMGQ LQGNLVSFRFVLSLFMHNLDHLTSGGAALRG  
Sbjct: 1229 CLGILLYLLQVPSFLANETPYKVMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 1050

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG 200  
GVHTDGGFFSCTCVLLPMHVYLGGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG  
Sbjct: 1049 GVHTDGGFFSCTCVLLPMHVYLGGLFCDVADGGPLLANNGTHILGGHQEPKGDVHLLLLG 870

Query: 199 WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLOGMVLQLVAIQLHDGSPG 29  
WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLOGMVLQLVAIQLHDG PG  
Sbjct: 869 WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLOGMVLQLVAIQLHDGLPG 699

Score = 527 bits (1145), Expect(3) = 0.0  
Identities = 225/227 (99%), Positives = 225/227 (99%)  
Frame = +2 / +3

Query: 32 RGAIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ 211  
R AIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ  
Sbjct: 702 RGAIMKLNQHLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ 881

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG 391  
QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG  
Sbjct: 882 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKASVHSTPEG 1061

Query: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI 571  
CSSACKMILEIMHKEAKDTKTADDEVPLK LAHNNFVGRIGKEGRNLKKVEQDTETKITI  
Sbjct: 1062 CSSACKMILEIMHKEAKDTKTADDEVPLKTLAHNNFVGRIGKEGRNLKKVEQDTETKITI 1241

Query: 572 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712  
SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS  
Sbjct: 1242 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1382

Score = 522 bits (1133), Expect(5) = 0.0  
Identities = 218/242 (90%), Positives = 220/242 (90%)  
Frame = -3 / -3

Query: 1583 PRGAXSVGPIGWVFGAXRSGFLTGTSTFSIKWANLIYSPAXVSRIPTHSQACRGEHTLDFC 1404  
P G +G +G GA RSGFLTGTSTFSIKWANLIYSPA VSRIPTHSQACRGEHTLDFC  
Sbjct: 2259 PEGQTVLGQLGRCLGAERSGFLTGTSTFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFC 2080

Query: 1403 PLLSWTXRDREGLVTXXXXXXXSDAAA\*PGPGCLGSSVEPSDWHNRV\*FSR\*PGR 1224  
PLLSWT RDREGLVT SDAAA\*PGPGCLGSSVEPSDWHNRV\*FSR\*PGR  
Sbjct: 2079 PLLSWTRRDREGLVTSFVPGPGYSVPSDAAA\*PGPGCLGSSVEPSDWHNRV\*FSR\*PGR 1900

Query: 1223 SHQSGLLVLPPLPSNSATRSPPFHLQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC 1044  
SHQSGLLVLPPLPSNSATRSPPFHLQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC  
Sbjct: 1899 SHQSGLLVLPPLPSNSATRSPPFHLQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC 1720

Query: 1043 HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG 864  
HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG  
Sbjct: 1719 HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG 1540

Query: 863 \*T 858  
\*T  
Sbjct: 1539 \*T 1534

Score = 510 bits (1108), Expect(6) = 0.0  
Identities = 210/225 (93%), Positives = 210/225 (93%)  
Frame = +3 / +1

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016  
PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP  
Sbjct: 1513 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1692

Query: 1017 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1196  
NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\*  
Sbjct: 1693 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1872

Query: 1197 YQETRPLMRTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLP 1376  
YQETRPLMRTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRH GSDQPLP  
Sbjct: 1873 YQETRPLMRTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDVTRPRHEGSDQPLP 2052

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD\*ERC 1511  
VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD\*ERC  
Sbjct: 2053 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD\*ERC 2187

Score = 504 bits (1094), Expect(5) = 0.0  
Identities = 194/194 (100%), Positives = 194/194 (100%)  
Frame = +1 / +2

Query: 715 SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHHR 894  
SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHHR  
Sbjct: 1391 SPDPWPEPGCCRSFPSFIQSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHHR 1570

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1074  
QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS  
Sbjct: 1571 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1750

Query: 1075 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRT 1254  
QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRT  
Sbjct: 1751 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRT 1930

Query: 1255 FLCQSDGSTEDPRH 1296  
FLCQSDGSTEDPRH  
Sbjct: 1931 FLCQSDGSTEDPRH 1972

Score = 482 bits (1046), Expect(6) = 0.0  
Identities = 196/213 (92%), Positives = 196/213 (92%)  
Frame = -1 / -1

Query: 1513 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334  
EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSL C  
Sbjct: 2189 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPSCLGLVT 2010

Query: 1333 XXXXXXXXXLGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR 1154  
LGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR  
Sbjct: 2009 LSLMLLLNLGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR 1830

Query: 1153 FSTFANDPASC\*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974  
FSTFANDPASC\*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG  
Sbjct: 1829 FSTFANDPASC\*CWHTYVGLQLHFL LGTKEVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1650

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875  
VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC  
Sbjct: 1649 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1551

Score = 395 bits (857), Expect(5) = 0.0  
Identities = 168/179 (93%), Positives = 169/179 (94%)  
Frame = -2 / -2

Query: 711 LMAATSFS\*ASRTFFIISCSALQQFS MAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 532  
LMAATSFS\*ASRTFFIISCSALQQFS MAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF  
Sbjct: 1381 LMAATSFS\*ASRTFFIISCSALQQFS MAPFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 1202

Query: 531 RFRPSLPMRRPTKLLWARIFRG TXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352  
RFRPSLPMRRPTKLLWAR+FRGT LCIISKIILQAEQPSGVECTLMAFSA  
Sbjct: 1201 RFRPSLPMRRPTKLLWARVFRGTSSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 1022

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE 175  
APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE  
Sbjct: 1021 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSR RGMSTCCCLAGAPAAATGE 845

Score = 374 bits (810), Expect(4) = 0.0  
Identities = 150/152 (98%), Positives = 150/152 (98%)  
Frame = -2 / -2

Query: 1539 G\*XIRVPHWNIFLNQVGKPDLP GPXVPD SHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH 1360  
G\* IRVPHWNIFLNQVGKPDLP GP VPDSHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH  
Sbjct: 2215 G\*EIRVPHWNIFLNQVGKPDLP GP GPVDPD SHSFSGLP GRAHSRFLPVVVLDSKGQGGAGH 2036

Query: 1359 FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGT TTSAA 1180  
FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGT TTSAA  
Sbjct: 2035 FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGT TTSAA 1856

Query: 1179 VKFCNSFTVPPLPMTRPAADAGTRMWVSSFT 1084  
VKFCNSFTVPPLPMTRPAADAGTRMWVSSFT  
Sbjct: 1855 VKFCNSFTVPPLPMTRPAADAGTRMWVSSFT 1760

Score = 269 bits (582), Expect(6) = 0.0  
Identities = 113/134 (84%), Positives = 113/134 (84%)  
Frame = -3 / -3

Query: 701 PHHSHRPPELSSLF PARPCNSRXXXXXXXXXQGCKG\*GLATRRW\*FLSRYLALPSSGSV 522  
PHHSHRPPELSSLF PARPCNSR QGCKG\*GLATRRW\*FLSRYLALPSSGSV  
Sbjct: 1371 PHHSHRPPELSSLF PARPCNSRWPPSQ\*WSSQGCKG\*GLATRRW\*FLSRYLALPSSGSV 1192

Query: 521 LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYAXXXXXXXXXXXXXPQGWSAH\*WLFQLHLR 342  
LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYA PQGWSAH\*WLFQLHLR  
Sbjct: 1191 LPCQ\*DALQSYYPGSSGEPQPFWCP\*PLYA\*SPRSSYKRRSSPQGWSAH\*WLFQLHLR 1012

Query: 341 SPSYARLSWTGSVL 300  
SPSYARLSWTGSVL  
Sbjct: 1011 SPSYARLSWTGSVL 970

Score = 247 bits (534), Expect(4) = 0.0  
Identities = 101/103 (98%), Positives = 103/103 (100%)  
Frame = -2 / -2

Query: 1020 NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841  
NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC  
Sbjct: 1696 NWASGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1517

Query: 840 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*E 712  
SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPG+R\*+  
Sbjct: 1516 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGVR\*D 1388

Score = 227 bits (491), Expect(6) = 0.0  
Identities = 98/99 (98%), Positives = 98/99 (98%)  
Frame = +3 / +1

Query: 414 SWRLCIKRLRTPKRLTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 593  
SWRLCIKRLRTPKRLTRFP\*R WPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP  
Sbjct: 1084 SWRLCIKRLRTPKRLTRFP\*RPWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 1263

Query: 594 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMMMWLP\* 710  
FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMMMWLP\*  
Sbjct: 1264 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMMMWLP\* 1380

Score = 223 bits (482), Expect(5) = 0.0  
Identities = 88/88 (100%), Positives = 88/88 (100%)  
Frame = +3 / +1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA 293  
HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA  
Sbjct: 784 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSFPGSWCPSMWVPLLARRGPPSA 963

Query: 294 TSQNRPSPR\*TCIGRRTQVQLKKPSVCT 377  
TSQNRPSPR\*TCIGRRTQVQLKKPSVCT  
Sbjct: 964 TSQNRPSPR\*TCIGRRTQVQLKKPSVCT 1047

Score = 196 bits (422), Expect(5) = 0.0  
Identities = 78/78 (100%), Positives = 78/78 (100%)  
Frame = +1 / +2

Query: 424 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603  
YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP  
Sbjct: 1094 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 1273

Query: 604 \*EDHHCEGGHRELLQGRA 657  
\*EDHHCEGGHRELLQGRA  
Sbjct: 1274 \*EDHHCEGGHRELLQGRA 1327

Score = 141 bits (303), Expect(4) = 0.0  
Identities = 54/56 (96%), Positives = 54/56 (96%)  
Frame = -2 / -1

Query: 1704 KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG 1537  
KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG  
Sbjct: 2381 KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG 2214

Score = 136 bits (291), Expect(5) = 0.0  
Identities = 60/71 (84%), Positives = 60/71 (84%)  
Frame = +1 / +2

Query: 1372 SLSLXVQDNNGQKSRVCSPRQA\*E\*VGIRDWAGL\*IRFAHLIEKDVPVRNPDL SAPNTH 1551  
SLSL VQDNNGQKSRVCSPRQA\*E\*VGIRDWAGL\*IRFAHLIEKDVPVRNPDL SAP  
Sbjct: 2048 SLSLRVQDNNGQKSRVCSPRQA\*E\*VGIRDWAGL\*IRFAHLIEKDVPVRNPDL SAPKHL 2227

Query: 1552 PIGPTLXAPRG 1584  
P P P G  
Sbjct: 2228 PNWPNTVCPSPG 2260

Score = 133 bits (284), Expect(3) = 0.0  
Identities = 53/55 (96%), Positives = 53/55 (96%)  
Frame = +2 / +1

Query: 1538 PQTPTQLAQHCXPLGVSEIXAQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV 1702  
PQTPTQLAQHC PLGVSEI AQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV  
Sbjct: 2215 PQTPTQLAQHCLPLGVSEILAQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV 2379

Score = 133 bits (284), Expect(6) = 0.0  
Identities = 52/54 (96%), Positives = 52/54 (96%)  
Frame = +3 / +2

Query: 1542 KHPPNWPNTVCPSPGCQKX\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 1703  
KH PNWPNTVCPSPGCQK \*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF  
Sbjct: 2219 KHLNWPNTVCPSPGCQKF\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 2380

Score = 132 bits (282), Expect(6) = 0.0  
Identities = 50/55 (90%), Positives = 50/55 (90%)  
Frame = +1 / +2

Query: 19 PQFTPGSHHEAWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 183  
P SHHEAWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC  
Sbjct: 689 PGADQASHHEAWPPVGEPCPEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 853

Score = 129 bits (276), Expect(3) = 4e-38  
Identities = 52/55 (94%), Positives = 53/55 (96%)  
Frame = +1 / +3



Query: 1540 PNTHTPIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF 1704  
PNT+PIGPTL APRGVRN SARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF  
Sbjct: 2217 PNTYPIGPTLSAPRGVRNSSARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF 2381

Score = 125 bits (268), Expect(6) = 0.0  
Identities = 45/45 (100%), Positives = 45/45 (100%)  
Frame = +1 / +2

Query: 250 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP 384  
VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP  
Sbjct: 920 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP 1054

Score = 117 bits (251), Expect(6) = 0.0  
Identities = 52/55 (94%), Positives = 52/55 (94%)  
Frame = -3 / -2

Query: 1703 KPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALXFLTPRGAXSVGPIGWVFG 1539  
KPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLAL FLTPRGA SVGPIG VFG  
Sbjct: 2380 KPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALEFLTPRGADSVGPIG\*VFG 2216

Score = 111 bits (238), Expect(5) = 0.0  
Identities = 44/46 (95%), Positives = 44/46 (95%)  
Frame = -1 / -3

Query: 1702 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF\*HPEGXTV 1565  
NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF\*HPEG TV  
Sbjct: 2379 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR\*NF\*HPEGQTV 2242

Score = 85.4 bits (180), Expect(5) = 0.0  
Identities = 31/31 (100%), Positives = 31/31 (100%)  
Frame = -2 / -2

Query: 129 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMMA 37  
FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMMA  
Sbjct: 799 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMMA 707

Score = 83.1 bits (175), Expect(5) = 0.0  
Identities = 35/36 (97%), Positives = 35/36 (97%)  
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 713  
AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQAR QVR  
Sbjct: 1496 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARGQVR 1389

Score = 81.2 bits (171), Expect(6) = 0.0  
Identities = 35/49 (71%), Positives = 35/49 (71%)  
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX\*WL 36  
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR \*WL  
Sbjct: 852 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS\*WL 706

Score = 56.5 bits (117), Expect(6) = 0.0  
Identities = 21/21 (100%), Positives = 21/21 (100%)  
Frame = -3 / -3

Query: 809 QPQ\*RCWEAAGLRWMKLGKDL 747  
QPQ\*RCWEAAGLRWMKLGKDL  
Sbjct: 1485 QPQ\*RCWEAAGLRWMKLGKDL 1423

Score = 42.8 bits (87), Expect(3) = 4e-38  
Identities = 13/37 (35%), Positives = 26/37 (70%)  
Frame = +2 / +3

Query: 461 EVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571  
++PL++L +VG +IGKEG ++ + + T++KI +  
Sbjct: 888 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 998

Score = 41.4 bits (84), Expect(2) = 6e-06  
Identities = 13/37 (35%), Positives = 25/37 (67%)  
Frame = +2 / +3

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDV 328  
++PL+ L +VG +IGKEG ++ + + T++KI +  
Sbjct: 1131 EVPLKTLAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 1241

Score = 40.9 bits (83), Expect(3) = 4e-38  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +3

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1785 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1916

Score = 40.9 bits (83), Expect(2) = 6e-06  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +3

Query: 1109 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1240  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1539 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1670

Score = 38.6 bits (78), Expect = 6.8  
Identities = 15/54 (27%), Positives = 30/54 (55%)  
Frame = +2 / +3

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012  
+++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
Sbjct: 897 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 1058

Score = 38.6 bits (78), Expect = 6.8  
Identities = 15/54 (27%), Positives = 30/54 (55%)  
Frame = +2 / +3

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388  
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
 Sbjct: 1527 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1688

Score = 35.4 bits (71), Expect(6) = 0.0  
 Identities = 11/11 (100%), Positives = 11/11 (100%)  
 Frame = -3 / -3

Query: 260 HPHTGWAPGAE 228  
 HPHTGWAPGAE  
 Sbjct: 930 HPHTGWAPGAE 898

Score = 30.4 bits (60), Expect(5) = 0.0  
 Identities = 12/13 (92%), Positives = 13/13 (100%)  
 Frame = +3 / +1

Query: 30 PGEPS\*S\*MATSW 68  
 PG+PS\*S\*MATSW  
 Sbjct: 700 PGKPS\*S\*MATSW 738

Score = 26.7 bits (52), Expect(6) = 0.0  
 Identities = 11/11 (100%), Positives = 11/11 (100%)  
 Frame = +3 / +1

Query: 747 \*VFSQLHPAQS 779  
 \*VFSQLHPAQS  
 Sbjct: 1423 \*VFSQLHPAQS 1455

>gi|7141071|gb|AF198254.1|AF198254 Homo sapiens mRNA-binding protein CRDBP m  
 Length = 2381

Score = 576 bits (1252), Expect(3) = 0.0  
 Identities = 251/279 (89%), Positives = 253/279 (90%)  
 Frame = +2 / +3

Query: 704 AMSSHLIPGLNLAAGVLFXXXXXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVG 883  
 ++ SHL PGLNLAAGVLF TGAAPYSSFMQAPEQEMVQVFIPAQAVG  
 Sbjct: 1380 SLQSHLTPGLNLAAGVLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 1559

Query: 884 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1063  
 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN  
 Sbjct: 1560 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEEN 1739

Query: 1064 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1243  
 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK  
 Sbjct: 1740 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 1919

Query: 1244 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRKXXXXXXXXXESRTTGRNRECA 1423  
 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRK ESRTTGRNRECA  
 Sbjct: 1920 IIGHFYASQMAQRKIRDILAQVKQHQKQGSNQAQARRK\*PAPPCPFESRTTGRNRECA 2099

Query: 1424 LPGRPENEWESGTXGPGCRSGLPT\*LRKMFQ\*GTLIXQP 1540

LPGRPENEWESGT GPGCRSGLPT\*LRKMFQ\*GTLI QP  
 Sbjct: 2100 LPGRPENEWESGTPGPGCRSGLPT\*LRKMFQ\*GTLI SQP 2216

Score = 555 bits (1206), Expect(4) = 0.0  
 Identities = 227/237 (95%), Positives = 232/237 (97%)  
 Frame = -1 / -1

Query: 739 QVQARDQVRAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 560  
 Q + + +++AHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF  
 Sbjct: 1409 QARGQVRLQAHGSHIILIGLPNLFHYFLLGPATILDGPLHSDGPLRVVKGKVLQRGDGDF 1230

Query: 559 CLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 380  
 CLGILLYLLQVPSFLANETPYKVIMGQ LQGNLVSFRFVLSLFMHNLDHLTSGGAALRG  
 Sbjct: 1229 CLGILLYLLQVPSFLANETPYKVIMGQGLQGNLVSFRFVLSLFMHNLDHLTSGGAALRG 1050

Query: 379 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG 200  
 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG  
 Sbjct: 1049 GVHTDGGFFSCTCVLLPMHVYLGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLG 870

Query: 199 WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGSPG 29  
 WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDG PG  
 Sbjct: 869 WGPRCHR\*ALAGLTPRAKAPSAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGLPG 699

Score = 527 bits (1145), Expect(3) = 0.0  
 Identities = 225/227 (99%), Positives = 225/227 (99%)  
 Frame = +2 / +3

Query: 32 RGAIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ 211  
 R AIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ  
 Sbjct: 702 RGAIMKLNGHQLENHALKVSYPDEQIAQGPENRRGGFGSRGQPRQGS PVAAGAPAKQQ 881

Query: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391  
 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG  
 Sbjct: 882 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 1061

Query: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI 571  
 CSSACKMILEIMHKEAKDTKTADDEVPLK LAHNNFVGRIGKEGRNLKKVEQDTETKITI  
 Sbjct: 1062 CSSACKMILEIMHKEAKDTKTADDEVPLKTLAHNNFVGRIGKEGRNLKKVEQDTETKITI 1241

Query: 572 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712  
 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS  
 Sbjct: 1242 SSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 1382

Score = 522 bits (1133), Expect(5) = 0.0  
 Identities = 218/242 (90%), Positives = 220/242 (90%)  
 Frame = -3 / -3

Query: 1583 PRGAXSVGPVGWVFGAXRSGFLTGTSTFSIKWANLIYSPA XVSRIPTH SQACRGEHTLDFC 1404  
 P G +G +G GA RSGFLTGTSTFSIKWANLIYSPA XVSRIPTH SQACRGEHTLDFC  
 Sbjct: 2259 PEGQTVLQGLGRCLGAERSGFLTGTSTFSIKWANLIYSPA QVSRIPTH SQACRGEHTLDFC 2080

Query: 1403 PLLSWTXRDREGLVTXXXXXXXXXXXXSDAAA\*PGPGCLGSSVEPSDWHNRV\*FSR\*PGR 1224

PLLSWT RDREGLVT SDAAA\*PGPGCLGSSVEPSDWHRNVR\*FSR\*PGR  
 Sbjct: 2079 PLLSWTRRDREGLVTSFVPGPGYSVPSDAAA\*PGPGCLGSSVEPSDWHRNVR\*FSR\*PGR 1900

Query: 1223 SHQGSGLLVLPQLPSNSATRSPPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC 1044  
 SHQGSGLLVLPQLPSNSATRSPPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC  
 Sbjct: 1899 SHQGSGLLVLPQLPSNSATRSPPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VC 1720

Query: 1043 HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG 864  
 HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG  
 Sbjct: 1719 HRFFPEP\*IGPLAVQ\*\*\*PYELWSQVFRVVQS\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG 1540

Query: 863 \*T 858  
 \*T  
 Sbjct: 1539 \*T 1534

Score = 510 bits (1108), Expect(6) = 0.0  
 Identities = 210/225 (93%), Positives = 210/225 (93%)  
 Frame = +3 / +1

Query: 837 PSRRWCRCCLSPPRQWAPXXXXXXXXXXXXXPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1016  
 PSRRWCRCCLSPPRQWAP PGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP  
 Sbjct: 1513 PSRRWCRCCLSPPRQWAPSSARRGSTSNSSPGLPAPPSRLHHPKHLTPKFVWLSSLDRQRP 1692

Query: 1017 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1196  
 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\*  
 Sbjct: 1693 NSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*TSCRI\*RQLRW\* 1872

Query: 1197 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHGGSDQPLP 1376  
 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRH GSDQPLP  
 Sbjct: 1873 YQETRPLMRTTRSS\*KSSDISMPVRWLNGRSETSWPRLSSSIRRDRVTRPRHEGSDQPLP 2052

Query: 1377 VPXSPGQQRAEIESVLSPAGLRMSGNPGHXGRAVDQVCPLD\*ERC 1511  
 VP SPGQQRAEIESVLSPAGLRMSGNPGH GRAVDQVCPLD\*ERC  
 Sbjct: 2053 VPSSPGQQRAEIESVLSPAGLRMSGNPGHLGRAVDQVCPLD\*ERC 2187

Score = 504 bits (1094), Expect(5) = 0.0  
 Identities = 194/194 (100%), Positives = 194/194 (100%)  
 Frame = +1 / +2

Query: 715 SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHR 894  
 SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHR  
 Sbjct: 1391 SPDPWPEPGCCRSFPSFIQRSPAASQQRYWGCSL\*LLYAGSRAGDGAGVYPRPGSGRHHR 1570

Query: 895 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1074  
 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS  
 Sbjct: 1571 QEGAAHQ TALPVCQRLHQDCTTRNT\*LQSSYGYHHWTARGPIQGSGKNLWQTQGGELLWS 1750

Query: 1075 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT 1254  
 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT  
 Sbjct: 1751 QGGSEAGDPHTCASISSWPQHWQRWKNGERVAEFDGS\*GGSTKRDPD\*\*ERPGHRENHRT 1930

Query: 1255 FLCQSDGSTEDPRH 1296

FLCQSDGSTEDPRH

Sbjct: 1931 FLCQSDGSTEDPRH 1972

Score = 482 bits (1046), Expect(6) = 0.0  
Identities = 196/213 (92%), Positives = 196/213 (92%)  
Frame = -1 / -1

Query: 1513 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334  
EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLP C  
Sbjct: 2189 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCGLGLVT 2010

Query: 1333 XXXXXXXXXXXLGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR 1154  
LGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR  
Sbjct: 2009 LSLMLLLNLGQDVSDLP LSHLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVHR 1830

Query: 1153 FSTFANDPASC\*CWHTYVGLQLHFLLGTKVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 974  
FSTFANDPASC\*CWHTYVGLQLHFLLGTKVLLLEFAIDSSLSLELGLWRSSDDNHTNFG  
Sbjct: 1829 FSTFANDPASC\*CWHTYVGLQLHFLLGTKVLLLEFAIDSSLSLELGLWRSSDDNHTNFG 1650

Query: 973 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 875  
VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC  
Sbjct: 1649 VRCFGWCNLDGGAGKPGELFDVLP LLADDGAHC 1551

Score = 395 bits (857), Expect(5) = 0.0  
Identities = 168/179 (93%), Positives = 169/179 (94%)  
Frame = -2 / -2

Query: 711 LMAATSFS\*ASRTFFIISCSALQQFSMAFFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 532  
LMAATSFS\*ASRTFFIISCSALQQFSMAFFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF  
Sbjct: 1381 LMAATSFS\*ASRTFFIISCSALQQFSMAFFTVMVLSGL\*RVRSCNEEMVIFVSVSCSTFF 1202

Query: 531 RFRPSLPMRRPTKLLWARIFRGTXXXXXXXXXXXLCIISKIILQAEQPSGVECTLMAFSA 352  
RFRPSLPMRRPTKLLWAR+FRGT LCIISKIILQAEQPSGVECTLMAFSA  
Sbjct: 1201 RFRPSLPMRRPTKLLWARVFRGTSSAVLVSLASLCIISKIILQAEQPSGVECTLMAFSA 1022

Query: 351 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE 175  
APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE  
Sbjct: 1021 APAFSFLCTSILDWVCFVMLRMVAPSLPIMAPTYWVGTRSRRMSTCCCLAGAPAATGE 845

Score = 374 bits (810), Expect(4) = 0.0  
Identities = 150/152 (98%), Positives = 150/152 (98%)  
Frame = -2 / -2

Query: 1539 G\*XIRVPHWNIFLNQVGKPDLP GPXVPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH 1360  
G\* IRVPHWNIFLNQVGKPDLP GP VPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH  
Sbjct: 2215 G\*EIRVPHWNIFLNQVGKPDLP GP GPVDPDSSHFSGLPGRAHSRFLPVVVLD SKGQGGAGH 2036

Query: 1359 FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAA 1180  
FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAA  
Sbjct: 2035 FLRAWAWLLCPF\*CCCLTWARMSRIFR\*AI\*LA\*KCPMIFTMTWSFSSGVWSLGTTSAA 1856

Query: 1179 VKFCNSFTVPPLPMTRPAADAGTRMWSSFT 1084

VKFCNSFTVFPPLPMTRPAADAGTRMWSSFT  
Sbjct: 1855 VKFCNSFTVFPPLPMTRPAADAGTRMWSSFT 1760

Score = 269 bits (582), Expect(6) = 0.0  
Identities = 113/134 (84%), Positives = 113/134 (84%)  
Frame = -3 / -3

Query: 701 PHHSHRPPELSSLFPARPCNNSRXXXXXXXXXXQGCKG\*GLATRRW\*FLSRYLALPSSGSV 522  
PHHSHRPPELSSLFPARPCNNSR QGCKG\*GLATRRW\*FLSRYLALPSSGSV  
Sbjct: 1371 PHHSHRPPELSSLFPARPCNNSRWPPSQ\*WSSQGCKG\*GLATRRW\*FLSRYLALPSSGSV 1192

Query: 521 LPCQ\*DALQSYYPGSSGEPRQPFWCP\*PLYAXXXXXXXXXXXXXPQGWSAH\*WLFQLHLR 342  
LPCQ\*DALQSYYPGSSGEPRQPFWCP\*PLYA PQGWSAH\*WLFQLHLR  
Sbjct: 1191 LPCQ\*DALQSYYPGSSGEPRQPFWCP\*PLYA\*SPRSSYKRRSSPQGWSAH\*WLFQLHLR 1012

Query: 341 SPSYARLSWTGSVL 300  
SPSYARLSWTGSVL  
Sbjct: 1011 SPSYARLSWTGSVL 970

Score = 247 bits (534), Expect(4) = 0.0  
Identities = 101/103 (98%), Positives = 103/103 (100%)  
Frame = -2 / -2

Query: 1020 NWSGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 841  
NWSGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC  
Sbjct: 1696 NWSGGPVMITIRTLESVSGGAILMEALANRESCLMCCPFLPMMAPTAWAGINTCTISC 1517

Query: 840 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*E 712  
SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPG+R\*+  
Sbjct: 1516 SGACIKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGVR\*D 1388

Score = 227 bits (491), Expect(6) = 0.0  
Identities = 98/99 (98%), Positives = 98/99 (98%)  
Frame = +3 / +1

Query: 414 SWRLCIKRLRTPKRLTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 593  
SWRLCIKRLRTPKRLTRFP\*R WPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP  
Sbjct: 1084 SWRLCIKRLRTPKRLTRFP\*RPWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPRCKTLP 1263

Query: 594 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGRPMMRWLP\* 710  
FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGRPMMRWLP\*  
Sbjct: 1264 FTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGRPMMRWLP\* 1380

Score = 223 bits (482), Expect(5) = 0.0  
Identities = 88/88 (100%), Positives = 88/88 (100%)  
Frame = +3 / +1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA 293  
HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA  
Sbjct: 784 HRDLRMGAEGALALGVSPARHLWQRGQPSSSKWTSPFGSWCPSMWWPLLARRGPPSA 963

Query: 294 TSQNRPSR\*TCIGRRTQVQLKKPSVCT 377

TSQNRPSPR\*TCIGRRTQVQLKKPSVCT  
Sbjct: 964 TSQNRPSPR\*TCIGRRTQVQLKKPSVCT 1047

Score = 196 bits (422), Expect(5) = 0.0  
Identities = 78/78 (100%), Positives = 78/78 (100%)  
Frame = +1 / +2

Query: 424 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 603  
YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP  
Sbjct: 1094 YA\*RG\*GHQNG\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLVARPYPLQP 1273

Query: 604 \*EDHHCEGGHRELLQGRA 657  
\*EDHHCEGGHRELLQGRA  
Sbjct: 1274 \*EDHHCEGGHRELLQGRA 1327

Score = 141 bits (303), Expect(4) = 0.0  
Identities = 54/56 (96%), Positives = 54/56 (96%)  
Frame = -2 / -1

Query: 1704 KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG 1537  
KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG  
Sbjct: 2381 KT\*RKFYFSSH\*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG 2214

Score = 136 bits (291), Expect(5) = 0.0  
Identities = 60/71 (84%), Positives = 60/71 (84%)  
Frame = +1 / +2

Query: 1372 SLSLXVQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH 1551  
SLSL VQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAP  
Sbjct: 2048 SLSLRVQDNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPKHL 2227

Query: 1552 PIGPTLXAPRG 1584  
P P P G  
Sbjct: 2228 PNWPNTVCPSPG 2260

Score = 133 bits (284), Expect(3) = 0.0  
Identities = 53/55 (96%), Positives = 53/55 (96%)  
Frame = +2 / +1

Query: 1538 PQTPTQLAQHCXPLGVSEIXAQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV 1702  
PQTPTQLAQHC PLGVSEI AQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV  
Sbjct: 2215 PQTPTQLAQHCLPLGVSEILAQGTFRGLFKEALQAPPRGWITPQWEEK\*NFLQV 2379

Score = 133 bits (284), Expect(6) = 0.0  
Identities = 52/54 (96%), Positives = 52/54 (96%)  
Frame = +3 / +2

Query: 1542 KHPPNWPNTVCPSPGCQKX\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 1703  
KH PNWPNTVCPSPGCQK \*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF  
Sbjct: 2219 KHLPNWPNTVCPSPGCQKF\*RKALLNVDCLKKLSRPHQEGGSHLSGKKNKISFRF 2380

Score = 132 bits (282), Expect(6) = 0.0



Identities = 50/55 (90%), Positives = 50/55 (90%)  
Frame = +1 / +2

Query: 19 PQFTPGSHHEAWPPVGEPCEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 183  
P SHHEAEWPPVGEPCEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC  
Sbjct: 689 PGADQASHHEAEWPPVGEPCEGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 853

Score = 129 bits (276), Expect(3) = 4e-38  
Identities = 52/55 (94%), Positives = 53/55 (96%)  
Frame = +1 / +3

Query: 1540 PNTHPIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF 1704  
PNT+PIGPTL APRGVRN SARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF  
Sbjct: 2217 PNTYPIGPTLSAPRGVRNSSARHF\*TWIV\*RSSPGPTKRVDHTSVGRKIKFPSGF 2381

Score = 125 bits (268), Expect(6) = 0.0  
Identities = 45/45 (100%), Positives = 45/45 (100%)  
Frame = +1 / +2

Query: 250 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP 384  
VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP  
Sbjct: 920 VCGCHYWQGGGHHHPQHHKTDVPVQDRRA\*EGERRCS\*KSHQCALHP 1054

Score = 117 bits (251), Expect(6) = 0.0  
Identities = 52/55 (94%), Positives = 52/55 (94%)  
Frame = -3 / -2

Query: 1703 KPEGNFIFLPTTEV\*STLLVGPCELL\*TIHV\*KCLALXFLTPRGAXSVGPIGWVFG 1539  
KPEGNFIFLPTTEV\*STLLVGPCELL\*TIHV\*KCLAL FLTPRGA SVGPIG VFG  
Sbjct: 2380 KPEGNFIFLPTTEV\*STLLVGPCELL\*TIHV\*KCLALEFLTPRGADSVGPIG\*VFG 2216

Score = 111 bits (238), Expect(5) = 0.0  
Identities = 44/46 (95%), Positives = 44/46 (95%)  
Frame = -1 / -3

Query: 1702 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF\*HPEGXTV 1565  
NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF\*HPEG TV  
Sbjct: 2379 NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR\*NF\*HPEGQTV 2242

Score = 85.4 bits (180), Expect(5) = 0.0  
Identities = 31/31 (100%), Positives = 31/31 (100%)  
Frame = -2 / -2

Query: 129 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 37  
FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA  
Sbjct: 799 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 707

Score = 83.1 bits (175), Expect(5) = 0.0  
Identities = 35/36 (97%), Positives = 35/36 (97%)  
Frame = -1 / -1

Query: 820 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 713

AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQAR QVR  
Sbjct: 1496 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARGQVR 1389

Score = 81.2 bits (171), Expect(6) = 0.0  
Identities = 35/49 (71%), Positives = 35/49 (71%)  
Frame = -3 / -3

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXXX\*WL 36  
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR \*WL  
Sbjct: 852 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS\*WL 706

Score = 56.5 bits (117), Expect(6) = 0.0  
Identities = 21/21 (100%), Positives = 21/21 (100%)  
Frame = -3 / -3

Query: 809 QPQ\*RCWEAAGLRWMKLGKDL 747  
QPQ\*RCWEAAGLRWMKLGKDL  
Sbjct: 1485 QPQ\*RCWEAAGLRWMKLGKDL 1423

Score = 42.8 bits (87), Expect(3) = 4e-38  
Identities = 13/37 (35%), Positives = 26/37 (70%)  
Frame = +2 / +3

Query: 461 EVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITI 571  
++PL++L +VG +IGKEG ++ + + T++KI +  
Sbjct: 888 DIPLRLLVPTQYVGAIIIGKEGATIRNITKQTQSKIDV 998

Score = 41.4 bits (84), Expect(2) = 6e-06  
Identities = 13/37 (35%), Positives = 25/37 (67%)  
Frame = +2 / +3

Query: 218 DIPLRLLVPTQYVGAIIIGKEGATIRNITKQTQSKIDV 328  
++PL+ L +VG +IGKEG ++ + + T++KI +  
Sbjct: 1131 EVPLKTLAHNNFVGRLIGKEGRNLKKVEQDTETKITI 1241

Score = 40.9 bits (83), Expect(3) = 4e-38  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +3

Query: 863 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 994  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1785 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1916

Score = 40.9 bits (83), Expect(2) = 6e-06  
Identities = 13/44 (29%), Positives = 26/44 (59%)  
Frame = +2 / +3

Query: 1109 VPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIV 1240  
+PA A G +IGK G+ + +L +A + + +TPD ++++  
Sbjct: 1539 IPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVI 1670

Score = 38.6 bits (78), Expect = 6.8

Identities = 15/54 (27%), Positives = 30/54 (55%)  
 Frame = +2 / +3

Query: 851 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1012  
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
 Sbjct: 897 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 1058

Score = 38.6 bits (78), Expect = 6.8  
 Identities = 15/54 (27%), Positives = 30/54 (55%)  
 Frame = +2 / +3

Query: 227 LRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPE 388  
 +++ +P Q VGAIIGK+G I+ +++ + I + E + + + + PE  
 Sbjct: 1527 VQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVIITGPPE 1688

Score = 35.4 bits (71), Expect(6) = 0.0  
 Identities = 11/11 (100%), Positives = 11/11 (100%)  
 Frame = -3 / -3


Query: 260 HPHTGWAPGAE 228  
 HPHTGWAPGAE  
 Sbjct: 930 HPHTGWAPGAE 898

Score = 30.4 bits (60), Expect(5) = 0.0  
 Identities = 12/13 (92%), Positives = 13/13 (100%)  
 Frame = +3 / +1

Query: 30 PGEPS\*S\*MATSW 68  
 PG+PS\*S\*MATSW  
 Sbjct: 700 PGKPS\*S\*MATSW 738

Score = 26.7 bits (52), Expect(6) = 0.0  
 Identities = 11/11 (100%), Positives = 11/11 (100%)  
 Frame = +3 / +1

Query: 747 \*VFSQLHPAQS 779  
 \*VFSQLHPAQS  
 Sbjct: 1423 \*VFSQLHPAQS 1455

>gi|24580458|gb|AC105030.11|  Homo sapiens chromosome 17, clone CTD-2244F11, comp  
 Length = 107848

Score = 363 bits (786), Expect(10) = 0.0  
 Identities = 142/146 (97%), Positives = 142/146 (97%)  
 Frame = -2 / +2

Query: 1707 FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCAXISDTPRGXQCWANWVGWVG\*XI 1528  
 FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCA ISDTPRG QCWANWVGWVG\* I  
 Sbjct: 72236 FKT\*RKIFYSSH\*GVIHPLGGAWRASLNNPRLKVPCARISDTPRGRQCWANWVGWVG\*EI 72415

Query: 1527 RVPHWNIFLNQVGKPDLPQGPXVPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA 1348  
 RVPHWNIFLNQVGKPDLPQGP VPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA  
 Sbjct: 72416 RVPHWNIFLNQVGKPDLPQGPVPDSHSFSGLPGRAHSRFLPVVVLDKSGQGGAGHFLRA 72595

Query: 1347 WAWLLCPF\*CCCLTWARMSRIFR\*AI 1270  
WAWLLCPF\*CCCLTWARMSRIFR\*AI  
Sbjct: 72596 WAWLLCPF\*CCCLTWARMSRIFR\*AI 72673

Score = 326 bits (706), Expect(10) = 0.0  
Identities = 133/146 (91%), Positives = 133/146 (91%)  
Frame = +3 / -3

Query: 1269 RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVPXSPGQQRAEIESVLSPAGLRMS 1448  
RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVP SPGQQRAEIESVLSPAGLRMS  
Sbjct: 72674 RWLNGRSETSWPRLSSSIRRDVTRPRHGGSDQPLPVPSSPGQQRAEIESVLSPAGLRMS 72495

Query: 1449 GNPGRHXGRAVDQVCPLD\*ERCXXXXXXXXXXKHPPNWPNTVCPSGCQKX\*RKALLNVDCL 1628  
GNPGRH GRAVDQVCPLD\*ERC KHPPNWPNTVCPSGCQK \*RKALLNVDCL  
Sbjct: 72494 GNPGRHLGRAVDQVCPLD\*ERCSSEEP\*SLSPKHPPNWPNTVCPSGCQKF\*RKALLNVDCL 72315

Query: 1629 KKLSRPHQEGGSHLSGKKNKISFRF\* 1706  
KKLSRPHQEGGSHLSGKKNKISFRF\*  
Sbjct: 72314 KKLSRPHQEGGSHLSGKKNKISFRF\* 72237

Score = 318 bits (688), Expect(12) = 0.0  
Identities = 135/147 (91%), Positives = 135/147 (91%)  
Frame = +2 / -2

Query: 1268 QMAQRKIRDILAQVKQHQKQSNQAQARRKXXXXXXXXXESRTTGRNRECALPGRPENE 1447  
QMAQRKIRDILAQVKQHQKQSNQAQARRK ESRTTGRNRECALPGRPENE  
Sbjct: 72675 QMAQRKIRDILAQVKQHQKQSNQAQARRK\*PAPPCPFESRTTGRNRECALPGRPENE 72496

Query: 1448 WESGTGXGPGCRSGLPT\*LRKMFQ\*GTLIQPTPTQLAQHCXPLGVSEIXAQGTFKRGLF 1627  
WESGT GPGCRSGLPT\*LRKMFQ\*GTLI QPPTPTQLAQHC PLGVSEI AQGTFKRGLF  
Sbjct: 72495 WESGTPGPGCRSGLPT\*LRKMFQ\*GTLIQPTPTPTQLAQHCLPLGVSEILAQGTFKRGLF 72316

Query: 1628 KEALQAPPRGWITPQWEEK\*NFLQVLK 1708  
KEALQAPPRGWITPQWEEK\*NFLQVLK  
Sbjct: 72315 KEALQAPPRGWITPQWEEK\*NFLQVLK 72235

Score = 303 bits (655), Expect(11) = 0.0  
Identities = 130/146 (89%), Positives = 130/146 (89%)  
Frame = -3 / +3

Query: 1706 LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALXFLTPRGAXSVGPIGWVFGAXRS 1527  
LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLAL FLTPRGA SVGPIGWVFGA RS  
Sbjct: 72237 LKPEGNFIFLPTEV\*STLLVGPGEELL\*TIHV\*KCLALEFLTPRGADSVGPIGWVFGAERS 72416

Query: 1526 GFLTGTSSFSIKWANLIYSPAXVSRIPTHSQACRGEHTLDFCPLLSWTXRDREGLVTXXXX 1347  
GFLTGTSSFSIKWANLIYSPA VSRIPTHSQACRGEHTLDFCPLLSWT RDREGLVT  
Sbjct: 72417 GFLTGTSSFSIKWANLIYSPAQVSRIPTHSQACRGEHTLDFCPLLSWTTRDREGLVTSSVP 72596

Query: 1346 XXXXXXXSDAAA\*PGPGCLGSSVEPS 1269  
SDAAA\*PGPGCLGSSVEPS  
Sbjct: 72597 GPGYSVPSDAAA\*PGPGCLGSSVEPS 72674

Score = 258 bits (557), Expect(9) = 0.0  
Identities = 109/112 (97%), Positives = 109/112 (97%)  
Frame = +1 / -1

Query: 1372 SLSLVQDNNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH 1551  
SLSL VQDNNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH  
Sbjct: 72571 SLSLRVQDNNNGQKSRVCSPRQA\*E\*VGIRDTWAGL\*IRFAHLIEKDVPVRNPDLAPNTH 72392

Query: 1552 PIGPTLXAPRGVRNXSARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK 1707  
PIGPTL APRGVRN SARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK  
Sbjct: 72391 PIGPTLSAPRGVRNSSARHF\*TWIV\*RSSPGPTKRDHTSVGRKIKFPSGFK 72236

Score = 232 bits (502), Expect(10) = 0.0  
Identities = 95/95 (100%), Positives = 95/95 (100%)  
Frame = -1 / +3

Query: 319 LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR\*ALAGLTPRAKAP 140  
LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR\*ALAGLTPRAKAP  
Sbjct: 83574 LGLGLFCDVADGGPLLANNNGTHILGGHQEPKGDVHLLLLGWGPRCHR\*ALAGLTPRAKAP 83753

Query: 139 SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS 35  
SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS  
Sbjct: 83754 SAPILRSLCYLLIGDVGDLQGMVLQLVAIQLHDGS 83858

Score = 223 bits (481), Expect(10) = 0.0  
Identities = 94/94 (100%), Positives = 94/94 (100%)  
Frame = +2 / -3

Query: 38 AIMKLNHGHQLENHALKVSYIPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV 217  
AIMKLNHGHQLENHALKVSYIPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV  
Sbjct: 83855 AIMKLNHGHQLENHALKVSYIPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQQV 83676

Query: 218 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK 319  
DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK  
Sbjct: 83675 DIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSK 83574

Score = 177 bits (380), Expect(9) = 0.0  
Identities = 68/68 (100%), Positives = 68/68 (100%)  
Frame = +3 / -1

Query: 114 HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA 293  
HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA  
Sbjct: 83779 HRDLRMGAEGALALGVSPARHLWQRGPQPSSSKWTSPFGSWCPPSMWVPLLARRGPPSA 83600

Query: 294 TSQNRPS 317  
TSQNRPS  
Sbjct: 83599 TSQNRPS 83576

Score = 156 bits (336), Expect(11) = e-177  
Identities = 66/82 (80%), Positives = 66/82 (80%)  
Frame = -1 / +1

Query: 1513 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLXGTGRGWSLPPCXXXXX 1334  
EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGL GTGRGWSLPPC  
Sbjct: 72430 EHLSQSSGQT\*STARPCPGFPLILRPAGESTLSISARCCPGLGTGRGWSLPPCLGLVT 72609

Query: 1333 XXXXXXXXXXXLGQDVSDLPLSHL 1268  
LGQDVSDLPLSHL  
Sbjct: 72610 LSLMLLLNLGQDVSDLPLSHL 72675

Score = 133 bits (286), Expect(12) = 0.0  
Identities = 50/51 (98%), Positives = 50/51 (98%)  
Frame = +1 / -2

Query: 31 PGSHHEAEWPPVGEPCEGGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 183  
P SHHEAEWPPVGEPCEGGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC  
Sbjct: 83862 PQSHHEAEWPPVGEPCEGGLLHPR\*ADSTGT\*EWAPRGLWLSGSAPPGLTC 83710

Score = 128 bits (274), Expect(10) = 0.0  
Identities = 46/46 (100%), Positives = 46/46 (100%)  
Frame = +1 / -1

Query: 1024 GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE 1161  
GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE  
Sbjct: 76135 GSGKNLWQTQGGELLWSQGGSEAGDPHTCASISSWPGHWQRWKNGE 75998

Score = 124 bits (266), Expect(11) = 0.0  
Identities = 48/48 (100%), Positives = 48/48 (100%)  
Frame = -2 / +1

Query: 318 LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE 175  
LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE  
Sbjct: 83575 LDWVCFVMLRMVAPSLPIMAPTYWVGTRSRGMSTCCCLAGAPAAATGE 83718

Score = 122 bits (260), Expect(10) = 0.0  
Identities = 46/46 (100%), Positives = 46/46 (100%)  
Frame = -3 / +3

Query: 1160 SPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRFFPEP 1023  
SPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRFFPEP  
Sbjct: 75999 SPFFHLCQ\*PGQLMLAHVCGSPASLPPWDQRSSPP\*VCHRFFPEP 76136

Score = 116 bits (249), Expect(10) = 0.0  
Identities = 46/47 (97%), Positives = 46/47 (97%)  
Frame = -1 / +2

Query: 454 RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVYLG 314  
RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVG  
Sbjct: 81932 RFGVLSLFMHNLDHLTSGGAALRGGVHTDGFFSCTCVLLPMHVYPG 82072

Score = 115 bits (246), Expect(11) = 0.0  
Identities = 47/49 (95%), Positives = 47/49 (95%)  
Frame = -1 / +1

Query: 1159 HRFSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLELG 1013  
HRFSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSL G  
Sbjct: 76000 HRFSTFANDPASC\*CWHTYVGLQLHFLLGTKEVLLLEFAIDSSLSLRRG 76146

Score = 115 bits (245), Expect(11) = e-177  
Identities = 46/48 (95%), Positives = 46/48 (95%)  
Frame = -1 / +1

Query: 1708 F\*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALRXNF\*HPEGXTV 1565  
F\*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR NF\*HPEG TV  
Sbjct: 72235 F\*NLKEILFFFPLRCDPPSWWGLESFFKQSTFKSALR\*NF\*HPEGQTV 72378

Score = 113 bits (242), Expect(10) = 0.0  
Identities = 46/47 (97%), Positives = 46/47 (97%)  
Frame = -1 / +3

Query: 712 AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQRG 572  
AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQ G  
Sbjct: 79647 AHGSHIILIGLPNFLHYFLLGPATILDGPLHSDGPLRVVKGKVLQPG 79787

Score = 110 bits (234), Expect(10) = 0.0  
Identities = 45/46 (97%), Positives = 46/46 (100%)  
Frame = +2 / -1

Query: 317 KIDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT 454  
+IDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT  
Sbjct: 82069 RIDVHRKENAGAAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKT 81932

Score = 109 bits (232), Expect(12) = 0.0  
Identities = 45/47 (95%), Positives = 47/47 (100%)  
Frame = +2 / -2

Query: 1022 KAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTVN 1162  
+AQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTV+  
Sbjct: 76137 QAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRVIKGGKTVS 75997

Score = 108 bits (230), Expect(9) = 0.0  
Identities = 47/49 (95%), Positives = 47/49 (95%)  
Frame = +3 / -3

Query: 1014 PNSRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\* 1160  
P RLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\*  
Sbjct: 76145 PLLRLREESMANSRRRTSLVPRRK\*SWRPTYVCQHQQLAGSLAKVEKR\* 75999

Score = 108 bits (230), Expect(10) = 0.0  
Identities = 45/45 (100%), Positives = 45/45 (100%)  
Frame = +2 / -3

Query: 578 LQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 712  
LQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS  
Sbjct: 79781 LQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS 79647

Score = 107 bits (228), Expect(10) = 0.0  
Identities = 40/43 (93%), Positives = 42/43 (97%)  
Frame = -2 / +2

Query: 948 LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGACIKE 820  
LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGAC ++  
Sbjct: 77939 LMEALANRESCLMCCPFLPMMAPTAWAGINTCTISCSGACCQD 78067

Score = 106 bits (227), Expect(10) = 0.0  
Identities = 42/42 (100%), Positives = 42/42 (100%)  
Frame = +1 / -2

Query: 454 G\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLV 579  
G\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLV  
Sbjct: 80646 G\*RGSPEDPGP\*\*LCRASHWQGRTEPEEGRARYRDKNHLLV 80521

Score = 106 bits (227), Expect(12) = 0.0  
Identities = 45/46 (97%), Positives = 45/46 (97%)  
Frame = +3 / -1

Query: 573 PRCKTLPFTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMRMMWLP\* 710  
P CKTLPFTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMRMMWLP\*  
Sbjct: 79786 PGCKTLPFTTLRGPSL\*RGPSRIVAGPSRK\*\*RKFGPRMRMMWLP\* 79649

Score = 105 bits (224), Expect(10) = 0.0  
Identities = 41/43 (95%), Positives = 42/43 (97%)  
Frame = +1 / -1

Query: 820 LLYAGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ 948  
+L AGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ  
Sbjct: 78067 ILAAGSRAGDGAGVYPRPGSGRHHRQEGAAHQ TALPVCQRLHQ 77939

Score = 103 bits (219), Expect(10) = 0.0  
Identities = 42/42 (100%), Positives = 42/42 (100%)  
Frame = -3 / +2

Query: 578 TRRW\*FLSRYLALPSSGSLVPCQ\*DALSYYGPGSSGEPRQP 453  
TRRW\*FLSRYLALPSSGSLVPCQ\*DALSYYGPGSSGEPRQP  
Sbjct: 80522 TRRW\*FLSRYLALPSSGSLVPCQ\*DALSYYGPGSSGEPRQP 80647

Score = 103 bits (219), Expect(10) = 0.0  
Identities = 38/38 (100%), Positives = 38/38 (100%)  
Frame = +1 / -2

Query: 715 SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL\*LLY 828  
SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL\*LLY  
Sbjct: 78588 SPDPWPEPGCCRSFPSFIQRSPAASQORYWGCSL\*LLY 78475

Score = 100 bits (213), Expect(11) = 0.0  
Identities = 41/41 (100%), Positives = 41/41 (100%)  
Frame = -1 / +3



Query: 577 RGDGDFCLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVS 455  
RGDGDFCLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVS  
Sbjct: 80523 RGDGDFCLGILLYLLQVPSFLANETPYKVIMGQDLQGNLVS 80645

Score = 100 bits (212), Expect(11) = 0.0  
Identities = 45/45 (100%), Positives = 45/45 (100%)  
Frame = -2 / +1

Query: 711 LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCN 577  
LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCN  
Sbjct: 79648 LMAATSFS\*ASRTFFIISCSALQQFSMAPFTVMVLSGL\*RVRSCN 79782

Score = 96.8 bits (205), Expect(10) = 0.0  
Identities = 38/39 (97%), Positives = 39/39 (100%)  
Frame = -1 / +3

Query: 1273 HLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH 1157  
+LTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH  
Sbjct: 75648 YLTGIEMSDDFHDDLVLIRGLVSWYYHLSCRQILQLVH 75764

Score = 96.4 bits (204), Expect(12) = 0.0  
Identities = 41/41 (100%), Positives = 41/41 (100%)  
Frame = +2 / -3

Query: 455 ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS 577  
ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS  
Sbjct: 80645 ADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISS 80523

Score = 95.5 bits (202), Expect(12) = 0.0  
Identities = 41/44 (93%), Positives = 43/44 (97%)  
Frame = +2 / -2

Query: 821 SFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKI 952  
S+ QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIK+  
Sbjct: 78066 SWQQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKV 77935

Score = 95.0 bits (201), Expect = 7e-17  
Identities = 40/49 (81%), Positives = 41/49 (83%)  
Frame = -3 / +2

Query: 1301 PGCLGSSVEPSDWHNRNVR\*FSR\*PGRSHQSGLLVLPPQLPSNSATRSP 1155  
P G + DWHNRNVR\*FSR\*PGRSHQSGLLVLPPQLPSNSATRSP  
Sbjct: 75620 PSLNGGAPYPVDWHNRNVR\*FSR\*PGRSHQSGLLVLPPQLPSNSATRSP 75766

Score = 94.1 bits (199), Expect(11) = e-177  
Identities = 38/38 (100%), Positives = 38/38 (100%)  
Frame = -2 / +1

Query: 576 EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT 463  
EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT  
Sbjct: 80524 EEMVIFVSVSCSTFFRFRPSLPMRRPTKLLWARIFRGT 80637

Score = 93.6 bits (198), Expect(10) = 0.0  
Identities = 38/38 (100%), Positives = 38/38 (100%)  
Frame = +1 / -2

Query: 1156 GERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRTFLCQS 1269  
GERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRTFLCQS  
Sbjct: 75765 GERVAEFDGS\*GGSTKRPDP\*\*ERPGHRENHRTFLCQS 75652

Score = 93.2 bits (197), Expect(11) = 0.0  
Identities = 38/38 (100%), Positives = 38/38 (100%)  
Frame = -2 / +1

Query: 1269 \*LA\*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT 1156  
\*LA\*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT  
Sbjct: 75652 \*LA\*KCPMIFTMTWSFSSGVWSLGTSTSAVKFCNSFT 75765

Score = 92.7 bits (196), Expect(9) = 0.0  
Identities = 41/41 (100%), Positives = 41/41 (100%)  
Frame = +3 / -1

Query: 456 LTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPR 578  
LTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPR  
Sbjct: 80644 LTRFP\*RSWPIITL\*GVSLARKDGT\*RR\*SKIPRQKSPSPR 80522

Score = 92.2 bits (195), Expect(12) = 0.0  
Identities = 39/43 (90%), Positives = 40/43 (93%)  
Frame = +2 / -3

Query: 1145 GGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQM 1273  
G VNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQ+  
Sbjct: 75776 GHPQVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQV 75648

Score = 90.0 bits (190), Expect(11) = 0.0  
Identities = 38/38 (100%), Positives = 38/38 (100%)  
Frame = -2 / +3

Query: 429 CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL 316  
CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL  
Sbjct: 81957 CIISKIILQAEEQPSGVECTLMAFSAAPAFSFLCTSIL 82070

Score = 89.5 bits (189), Expect(9) = 0.0  
Identities = 39/41 (95%), Positives = 41/41 (100%)  
Frame = +3 / -1

Query: 1155 R\*TSCRI\*RQLRW\*YQETRPLMRTRRSS\*KSSDISMPVRWL 1277  
R\*TSCRI\*RQLRW\*YQETRPLMRTRRSS\*KSSDISMPVR++  
Sbjct: 75766 R\*TSCRI\*RQLRW\*YQETRPLMRTRRSS\*KSSDISMPVRYI 75644

Score = 88.1 bits (186), Expect(10) = 0.0  
Identities = 38/39 (97%), Positives = 39/39 (100%)  
Frame = -2 / +1

Query: 828 IKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*E 712  
IKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*+  
Sbjct: 78475 IKEL\*GAAPVTLLGGGGTALDEAGKRPTAARFRPGIR\*D 78591

Score = 86.3 bits (182), Expect(11) = 0.0  
Identities = 36/36 (100%), Positives = 36/36 (100%)  
Frame = -1 / +3

Query: 820 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 713  
AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR  
Sbjct: 78483 AIGSSPSNAAGRRRDCAG\*SWEKTYSSQVQARDQVR 78590

Score = 85.8 bits (181), Expect(11) = e-177  
Identities = 35/49 (71%), Positives = 35/49 (71%)  
Frame = -3 / +1

Query: 461 RQPFWCP\*PLYAXXXXXXXXXXXXXX PQGWSAH\*WLFQLHLRSPSYARLSW 315  
R FWCW\*PLYA PQGWSAH\*WLFQLHLRSPSYARLSW  
Sbjct: 81925 RLTFWCW\*PLYA\*SPRSSYKRRSSP PQGWSAH\*WLFQLHLRSPSYARLSW 82071

Score = 85.4 bits (180), Expect(11) = 0.0  
Identities = 31/31 (100%), Positives = 31/31 (100%)  
Frame = -2 / +1

Query: 129 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 37  
FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA  
Sbjct: 83764 FSGPCAICSSGM\*ETFRAWFSNWWPFSFMMA 83856

Score = 82.2 bits (173), Expect(11) = e-177  
Identities = 36/51 (70%), Positives = 36/51 (70%)  
Frame = -3 / +2

Query: 182 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRXXXXXXXXXXXXXXXXX\*WLP G 30  
QVSPGGADPESQSPLGAHSQVPVLSAHRGCRR \*W L G  
Sbjct: 83711 QVSPGGADPESQSPLGAHSQVPVLSAHRGCRRPSGHGSPTGGHSAS\*WLWG 83863

Score = 79.0 bits (166), Expect(11) = e-177  
Identities = 33/42 (78%), Positives = 33/42 (78%)  
Frame = -3 / +2

Query: 701 PHHSHRPPELSSLFPARPCNNRXXXXXXXXXXQGCKG\*GLAT 576  
PHHSHRPPELSSLFPARPCNNR QGCKG\*GLAT  
Sbjct: 79658 PHHSHRPPELSSLFPARPCNNRWPPSQ\*WSSQGCKG\*GLAT 79783

Score = 77.6 bits (163), Expect(11) = 0.0  
Identities = 30/30 (100%), Positives = 30/30 (100%)  
Frame = -3 / +3

Query: 947 \*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T 858  
\*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T  
Sbjct: 77940 \*WRRWQTGRAV\*CAAPSCR\*WRPLPGRG\*T 78029

 **NCBI**  
Nucleotide      Protein      Translations      Retrieve results for an RID

*formatting* **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

SEQ 5  
translated → translation  
dp  
(blastx)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions  Alignments

Alignment view

Limit results by  or select from:

Expect value  range:



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

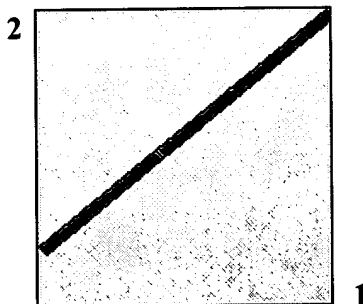
## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

SEQ 5  
gi 4191607 (IGFII)

Sequence 1 lcl|seq\_1 Length 1708 (1 .. 1708)

Sequence 2 lcl|seq\_2 Length 2130 (1 .. 2130)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3163 bits (1645), Expect = 0.0  
 Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)  
 Strand = Plus / Plus

```

Query: 37   agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 96
           |||
Sbjct: 411  agccatcatgaagctgaatggccaccagttggagaaccatgccctgaaggtctcctacat 470

Query: 97   ccccgatgagcagatagcacagggacctgagaatggcgccgagggggctttggctctcg 156
           |||
Sbjct: 471  ccccgatgagcagatagcacagggacctgagaatggcgccgagggggctttggctctcg 530

Query: 157  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaagcagcagcaagt 216
           |||
Sbjct: 531  gggtcagccccgccagggtcacctgtggcagcgggggccccagccaagcagcagcaagt 590

Query: 217  ggacatcccccttcgggtcctggtgccaccagtatgtgggtgccattattggcaagga 276
           |||
Sbjct: 591  ggacatcccccttcgggtcctggtgccaccagtatgtgggtgccattattggcaagga 650

Query: 277  gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa 336
           |||

```

Sbjct: 651 gggggccaccatccgcaacatcacaaaacagaccaggtccaagatagacgtgcataggaa 710

Query: 337 ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccctgagggctgctc 396  
|||||  
Sbjct: 711 ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccctgagggctgctc 770

Query: 397 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacccaaacggc 456  
|||||  
Sbjct: 771 ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacacccaaacggc 830

Query: 457 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgctctcattggcaa 516  
|||||  
Sbjct: 831 tgacgaggttcccctgaagatcctggcccataataactttgtagggcgctctcattggcaa 890

Query: 517 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 576  
|||||  
Sbjct: 891 ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc 950

Query: 577 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 636  
|||||  
Sbjct: 951 gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga 1010

Query: 637 gaattgttgaggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatga 696  
|||||  
Sbjct: 1011 gaattgttgaggccgagcaggaaataatgaagaaagttcgggaggcctatgagaatga 1070

Query: 697 tgtggctgcatgagc-----tctcacctgatccctggcctgaacctggctgctgtagg 750  
|||||  
Sbjct: 1071 tgtggctgcatgagcctgcagctctcacctgatccctggcctgaacctggctgctgtagg 1130

Query: 751 tcttttcccagcttcatccagcgcagtcgccgcctcccagcagcggttactggggctgc 810  
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Sbjct: 1131 tcttttcccagcttcatccagcgcagtcgccgcctcccagcagcggttactggggctgc 1190

Query: 811 tccctatagctcctttatgcaggctcccgagcaggagatggtgcaggtgtttatccccgc 870  
|||||  
Sbjct: 1191 tccctatagctcctttatgcaggctcccgagcaggagatggtgcaggtgtttatccccgc 1250

Query: 871 ccaggcagtgggcgccatcatcggaagaaggggcagcacatcaaacagctctcccggtt 930  
|||||  
Sbjct: 1251 ccaggcagtgggcgccatcatcggaagaaggggcagcacatcaaacagctctcccggtt 1310

Query: 931 tgccagcgctccatcaagattgcaccaccgaaacacctgactccaaagttcgtatggt 990  
|||||  
Sbjct: 1311 tgccagcgctccatcaagattgcaccaccgaaacacctgactccaaagttcgtatggt 1370

Query: 991 tatcatcactggaccgccagaggcccaattcaaggctcaggaagaatctatggcaaact 1050  
|||||  
Sbjct: 1371 tatcatcactggaccgccagaggcccaattcaaggctcaggaagaatctatggcaaact 1430

Query: 1051 caaggaggagaacttctttggtcccaaggaggaagtgaagctggagacccacatacgtgt 1110  
|||||

Sbjct: 1431 caaggaggagaacttctttggtcccaaggaggaagtgaagctggagacccacatacgtgt 1490

Query: 1111 gccagcatcagcagctggccgggtcattggcaaagggtggaaaaacgggtgaacgagttgca 1170  
|||||

Sbjct: 1491 gccagcatcagcagctggccgggtcattggcaaagggtggaaaaacgggtgaacgagttgca 1550

Query: 1171 gaatttgacggcagctgaggtggttagtaccaagagaccagaccctgatgagaacgacca 1230  
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Sbjct: 1551 gaatttgacggcagctgaggtggttagtaccaagagaccagaccctgatgagaacgacca 1610

Query: 1231 ggtcatcgtgaaaatcatcggacatttctatgccagtcagatggctcaacggaagatccg 1290  
|||||

Sbjct: 1611 ggtcatcgtgaaaatcatcggacatttctatgccagtcagatggctcaacggaagatccg 1670

Query: 1291 agacatcctggcccaggttaagcagcagcatcagaaggacagagtaaccaggcccaggc 1350  
|||||

Sbjct: 1671 agacatcctggcccaggttaagcagcagcatcagaaggacagagtaaccaggcccaggc 1730

Query: 1351 acggaggaagtgaccagcccctccctgtcccttcgagtcaggacaacaacgggcagaaa 1410  
|||||

Sbjct: 1731 acggaggaagtgaccagcccctccctgtcccttcgagtcaggacaacaacgggcagaaa 1790

Query: 1411 tcgagagtgtgctctccccggcaggcctgagaatgagtgggaatccgggacacctgggcc 1470  
|||||

Sbjct: 1791 tcgagagtgtgctctccccggcaggcctgagaatgagtgggaatccgggacacctgggcc 1850

Query: 1471 gggctgtagatcaggtttgccacttgattgagaaagatgttcagtgaggaaccctgat 1530  
|||||

Sbjct: 1851 gggctgtagatcaggtttgccacttgattgagaaagatgttcagtgaggaaccctgat 1910

Query: 1531 ctctcagccccaaacacccacccaattggcccaacactgtctgccctcgggggtgtcaga 1590  
|||||

Sbjct: 1911 ctctcagccccaaacacccacccaattggcccaacactgtctgccctcgggggtgtcaga 1970

Query: 1591 aattttagcgcaaggcacttttaaacgtggattgtttaaagaagctctccaggccccacc 1650  
|||||

Sbjct: 1971 aattttagcgcaaggcacttttaaacgtggattgtttaaagaagctctccaggccccacc 2030

Query: 1651 aagaggggtggatcacacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 1708  
|||||

Sbjct: 2031 aagaggggtggatcacacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 2088

CPU time: 0.01 user secs. 0.02 sys. secs 0.03 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 12

Number of Sequences: 0  
Number of extensions: 12  
Number of successful extensions: 2  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 1708  
length of database: 8,918,056,233  
effective HSP length: 25  
effective length of query: 1683  
effective length of database: 8,918,056,208  
effective search space: 15009088598064  
effective search space used: 15009088598064  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)





# results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061911853-27554-2290282.BLASTQ3

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,886,208 sequences; 8,918,056,233 total letters

seq 7

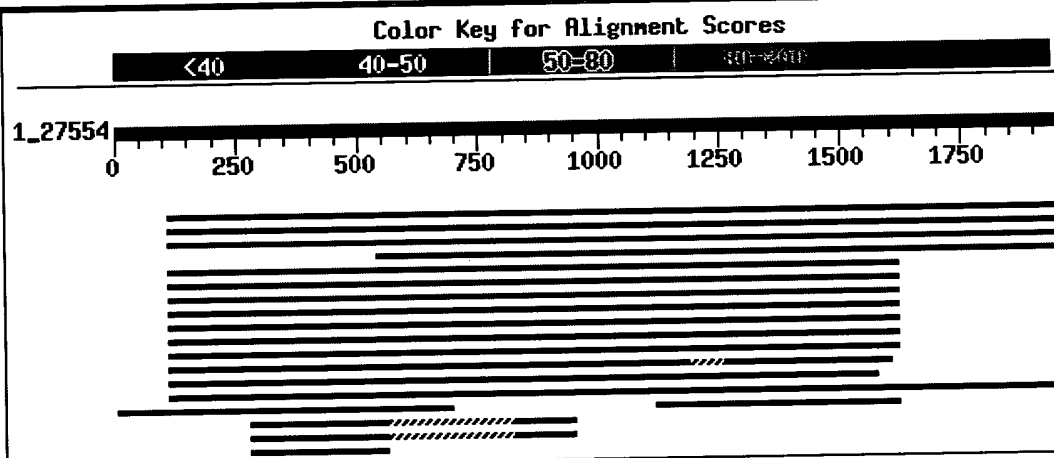
## Taxonomy reports

Query=

(1946 letters)

## Distribution of 39 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

gi 4191607 gb AF117106.1 AF117106	Homo sapiens IGF-II mRNA-...	3488	0.0
gi 21361351 ref NM 006546.2	Homo sapiens IGF-II mRNA-bind...	3451	0.0
gi 7141071 gb AF198254.1 AF198254	Homo sapiens mRNA-binding...	3451	0.0
gi 22760672 dbj AK074915.1	Homo sapiens cDNA FLJ90434 fis...	2663	0.0
gi 31342209 ref NM 175594.2	Rattus norvegicus IGF-II mRNA-...	1950	0.0
gi 27464837 gb AF541940.1	Rattus norvegicus b-actin zipcod...	1950	0.0
gi 3273748 gb AF061569.1 AF061569	Mus musculus coding regio...	1892	0.0
gi 31560605 ref NM 009951.2	Mus musculus insulin-like grow...	1886	0.0
gi 12851513 dbj AK013940.1	Mus musculus 13 days embryo hea...	1886	0.0
gi 26336870 dbj AK044850.1	Mus musculus 9.5 days embryo pa...	1886	0.0
gi 30354043 gb BC051679.1	Mus musculus insulin-like growth...	1886	0.0
gi 27689046 ref XM 220886.1	Rattus norvegicus similar to I...	1367	0.0
gi 2570920 gb AF026527.1 AF026527	Gallus gallus zipcode-bin...	1327	0.0
gi 24580458 gb AC105030.11	Homo sapiens chromosome 17, clo...	829	0.0
gi 21637524 gb AC091133.11	Homo sapiens chromosome 17, clo...	544	e-151
gi 30581644 gb AC094527.7	Rattus norvegicus 5 BAC CH230-4L...	477	e-131
gi 21954991 gb AC098642.5	Genomic sequence for Mus musculu...	342	1e-90

gi 14475918 gb AC084407.10	Mus Musculus Strain C57BL6/J Ch...	342	1e-90
gi 22204252 emb AL606704.20	Mouse DNA sequence from clone ...	342	1e-90

## Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1)  
Length = 2130

Score = 3488 bits (1814), Expect = 0.0  
Identities = 1834/1845 (99%), Gaps = 6/1845 (0%)  
Strand = Plus / Plus

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Sbjct: 244  aggagccggaattcaaatccgaaatattccacccagctccgatgggaagtactggac 303

Query: 168  agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227
          |||
Sbjct: 304  agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 363

Query: 228  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
          |||
Sbjct: 364  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 423

Query: 288  ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 347
          |||
Sbjct: 424  ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 483

Query: 348  atagcacagggacctgagaatgggcgccgagggggctttggctctcggggtcagccccgc 407
          |||
Sbjct: 484  atagcacagggacctgagaatgggcgccgagggggctttggctctcggggtcagccccgc 543

Query: 408  cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 467
          |||
Sbjct: 544  cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 603

Query: 468  cggctcctggtgcccaccagtatgtgggtgccattattggcaaggagggggccaccatc 527
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Sbjct: 604  cggctcctggtgcccaccagtatgtgggtgccattattggcaaggagggggccaccatc 663

Query: 528  cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggt 587
          |||
Sbjct: 664  cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggt 723

Query: 588  gcagctgaaaaagccatcagtgtgcactccaccctgagggctgctcctccgcttgaag 647
          |||
Sbjct: 724  gcagctgaaaaagccatcagtgtgcactccaccctgagggctgctcctccgcttgaag 783

Query: 648  atgatcttgagattatgcataaagaggctaaggacacccaaacggctgacgaggttccc 707
          |||
Sbjct: 784  atgatcttgagattatgcataaagaggctaaggacacccaaacggctgacgaggttccc 843

Query: 708  ctgaagatcctggccataataactttgtagggcgctctcattggcaaggaaggacggaac 767
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```

Sbjct: 844 ctgaagatcctggcccataataactttgtagggcgtctcattggcaaggaaggacggaac 903

Query: 768 ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcggtgcaagacctt 827  
|||||

Sbjct: 904 ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcggtgcaagacctt 963

Query: 828 accctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagg 887  
|||||

Sbjct: 964 accctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagg 1023

Query: 888 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 947  
|||||

Sbjct: 1024 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 1083

Query: 948 a<sup>f</sup>--gc--tctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct 1001  
| |||

Sbjct: 1084 agcctgcagtctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct 1143

Query: 1002 tcatccagcgcagtcctccgcgcctcccagcagcgttactggggctgctccctatagctcc 1061  
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Sbjct: 1144 tcatccagcgcagtcctccgcgcctcccagcagcgttactggggctgctccctatagctcc 1203

Query: 1062 tttatgcaggctcccgcagcaggagatggtgcagggtgttatccccgcccaggcagtgggc 1121  
|||||

Sbjct: 1204 tttatgcaggctcccgcagcaggagatggtgcagggtgttatccccgcccaggcagtgggc 1263

Query: 1122 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1181  
|||||

Sbjct: 1264 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1323

Query: 1182 atcaagattgcaccacccgaaacacctgactccaaagttcgtatgggttatcatcactgga 1241  
|||||

Sbjct: 1324 atcaagattgcaccacccgaaacacctgactccaaagttcgtatgggttatcatcactgga 1383

Query: 1242 ccgccagaggcccaattcaagggtcaggggaagaatctatggcaaactcaaggaggagaac 1301  
|||||

Sbjct: 1384 ccgccagaggcccaattcaagggtcaggggaagaatctatggcaaactcaaggaggagaac 1443

Query: 1302 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1361  
|||||

Sbjct: 1444 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1503

Query: 1362 gctggccgggtcatttgcaaggtggaaaaacggtgaacgagttgcagaatttgacggca 1421  
|||||

Sbjct: 1504 gctggccgggtcatttgcaaggtggaaaaacggtgaacgagttgcagaatttgacggca 1563

Query: 1422 gctgaggtggtagtaccaagagaccagaccctgatgagaacgaccaggtcatcgtgaaa 1481  
|||||

Sbjct: 1564 gctgaggtggtagtaccaagagaccagaccctgatgagaacgaccaggtcatcgtgaaa 1623

Query: 1482 atcatcggacatttctatgccagtcagatggctcaacggaagatccgagacatcctggcc 1541  
|||||

Sbjct: 1624 atcatcggacatttctatgccagtcagatggctcaacggaagatccgagacatcctggcc 1683

Query: 1542 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaggaagtga 1601  
|||||

Sbjct: 1684 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaggaagtga 1743

Query: 1602 ccagccccctccctgtcccttngagtccaggacaacaacgggcagaaatcgagagtgtgct 1661  
|||||

Sbjct: 1744 ccagccccctccctgtcccttcgagtccaggacaacaacgggcagaaatcgagagtgtgct 1803

Query: 1662 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggccgggctgtagatca 1721  
|||||

Sbjct: 1804 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggccgggctgtagatca 1863

Query: 1722 ggtttgcccacttgattgagaaagatgttccagtgaggaaccctgatctntcagccccc 1781  
|||||

Sbjct: 1864 ggtttgcccacttgattgagaaagatgttccagtgaggaaccctgatctntcagccccc 1923

Query: 1782 acaccacccaattggcccaacactgtntgccctcgggggtgtcagaaattntagcgcaa 1841  
|||||

Sbjct: 1924 acaccacccaattggcccaacactgtctgccctcgggggtgtcagaaattctagcgcaa 1983

Query: 1842 ggccacttttaaacgtggattgtttaagaagctctccaggccccaccaagagggtggatc 1901  
|||||

Sbjct: 1984 ggccacttttaaacgtggattgtttaagaagctctccaggccccaccaagagggtggatc 2043

Query: 1902 acacctcagtgggaagaaaaataaaatttccttcagggttttaaaa 1946  
|||||

Sbjct: 2044 acacctcagtgggaagaaaaataaaatttccttcagggttttaaaa 2088

>gi|21361351|ref|NM\_006546.2| Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1), mR  
Length = 2381

Score = 3451 bits (1795), Expect = 0.0  
Identities = 1826/1842 (99%), Gaps = 7/1842 (0%)  
Strand = Plus / Plus

Query: 108 aggagccggaaaaattcaaattccgaaatattccaccccagctccgatgggaagtactggac 167  
|||||

Sbjct: 540 aggagccggaaaaattcaaattccgaaatattccaccccagctccgatgggaagtactggac 599

Query: 168 agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaacaccgagagttag 227  
|||||

Sbjct: 600 agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaacaccgagagttag 659

Query: 228 acggcagtggtgaatgtcacctattccaacggggagcagaccaggcaagccatcatgaag 287  
|||||

Sbjct: 660 acggcagtggtgaatgtcacctattccaacggggagcagaccaggcaagccatcatgaag 719

Query: 288 ctgaatggccaccagttggagaacctatgccctgaagggtctcctacatccccgatgagcag 347  
|||||

Sbjct: 720 ctgaatggccaccagttggagaacctatgccctgaagggtctcctacatccccgatgagcag 779

Query: 348 atagcacagggacctgagaatgggcgcgcgagggggctttggctctcggggtcagccccgc 407  
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Sbjct: 780 atagcacagggacctgagaatgggcgcgcgagggggctttggctctcggggtcagccccgc 839

Query: 408 cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 467  
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Sbjct: 840 cagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccctt 899

Query: 468 cggctcctggtgccaccagctatgtgggtgccattattggcaaggagggggccaccatc 527  
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Sbjct: 900 cggctcctggtgccaccagctatgtgggtgccattattggcaaggagggggccaccatc 959

Query: 528 cgcaacatcacaaaacagaccagctccaagatagacgtgcataggaaggagaacgcaggt 587  
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Sbjct: 960 cgcaacatcacaaaacagaccagctccaagatagacgtgcataggaaggagaacgcaggt 1019

Query: 588 gcagctgaaaaagccatcagtggtgactccaccctgagggctgctcctccgcttgtaag 647  
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Sbjct: 1020 gcagctgaaaaagccatcagtggtgactccaccctgagggctgctcctccgcttgtaag 1079

Query: 648 atgatcttgagattatgcataaagaggctaaggacacccaaacggctgacgaggttccc 707  
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Sbjct: 1080 atgatcttgagattatgcataaagaggctaaggacacccaaacggctgacgaggttccc 1139

Query: 708 ctgaagatcctggcccataataactttgtagggcgtctcattggcaaggaaggacggaac 767  
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Query: 888 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 947  
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Sbjct: 1320 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 1379

Query: 948 a----gc--tctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct 1001  
| |  
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Sbjct: 1440 tcatccagcgcagtcgccgcctcccagcagcgttactggggctgctccctatagctcc 1499

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Query: 1122 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1181  
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Sbjct: 1560 gccatcatcggcaagaaggggcagcacatcaaacagctctcccggtttgccagcgcctcc 1619

Query: 1182 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggttatcatcactgga 1241  
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Sbjct: 1620 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggttatcatcactgga 1679

Query: 1242 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactcaaggaggagaac 1301  
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Sbjct: 1680 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactcaaggaggagaac 1739

Query: 1302 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1361  
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Sbjct: 1740 ttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagca 1799

Query: 1362 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcagaatttgacggca 1421  
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Sbjct: 1800 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcagaatttgacggca 1859

Query: 1422 gctgaggtggtagtagtaagagaccagacccctgatgagaacgaccaggtcatcgtgaaa 1481  
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Sbjct: 1860 gctgaggtggtagtagtaagagaccagacccctgatgagaacgaccaggtcatcgtgaaa 1919

Query: 1482 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgagacatcctggcc 1541  
|||  
Sbjct: 1920 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgagacatcctggcc 1979

Query: 1542 cagggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaaggaagtga 1601  
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Sbjct: 1980 cagggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacgaaggaagtga 2039

Query: 1602 ccagcccctccctgtcccttngagtccaggacaacaacgggcagaaatcgagagtgtgct 1661  
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Sbjct: 2040 ccagcccctccctgtcccttngagtccaggacaacaacgggcagaaatcgagagtgtgct 2099

Query: 1662 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggcccgggctgtagatca 1721  
|||  
Sbjct: 2100 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggcccgggctgtagatca 2159

Query: 1722 ggtttgcccacttgattgagaaagatgttccagtgaggaaccctgatctntcagcccc-a 1780  
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Sbjct: 2160 ggtttgcccacttgattgagaaagatgttccagtgaggaaccctgatctctcagccccca 2219

Query: 1781 aacacccaccaattggcccaacactgtntgcccctcggggtgtcagaaattntagcgca 1840  
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Query: 1841 aggcacttttaaacgtggattgtttaagaagctctccaggccccaccaagaggggtggat 1900  
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Sbjct: 2280 aggcacttttaaacgtggattgtttaagaagctctccaggccccaccaagaggggtggat 2339

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Sbjct: 2340 cacacctcagtgggaagaaaaataaaatttccttcaggtttt 2381

>gi|7141071|gb|AF198254.1|AF198254 Homo sapiens mRNA-binding protein CRDBP mRNA, com  
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Identities = 1826/1842 (99%), Gaps = 7/1842 (0%)  
Strand = Plus / Plus

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Sbjct: 540 aggagccggaaaattcaaattccgaaatattccacccagctccgatgggaagtactggac 599

Query: 168 agcctgctggctcagtattggtacagtagagaactgtgagcaagtgaacaccgagagtggag 227  
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Sbjct: 600 agcctgctggctcagtattggtacagtagagaactgtgagcaagtgaacaccgagagtggag 659

Query: 228 acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287  
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Sbjct: 660 acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 719

Query: 288 ctgaatggccaccagttggagaacctatgcctgaaggtctcctacatccccgatgagcag 347  
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Query: 348 atagcacagggacctgagaatgggcgcccagggggccttggctctcggggtcagccccgc 407  
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Query: 528 cgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcaggt 587  
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Query: 888 gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg 947
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Query: 1542 caggttaagcagcagcatcagaagggacagagtaaccaggcccaggcacggaggaagtga 1601  
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Sbjct: 2160 ggtttgcccacttgattgagaaagatgttccagtgaggaaccctgatctctcagccccca 2219

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Query: 1901 cacacctcagtgggaagaaaaataaaatttccttcagggtttt 1942  
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>gi|22760672|dbj|AK074915.1| Homo sapiens cDNA FLJ90434 fis, clone NT2RP3000789, hig  
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Length = 2780

Score = 2663 bits (1385), Expect = 0.0  
Identities = 1405/1416 (99%), Gaps = 6/1416 (0%)  
Strand = Plus / Plus

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Query: 597 aaagccatcagtgtgcactccaccctgagggtgctcctccgcttgtaagatgatcttg 656  
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Sbjct: 61 aaagccatcagtgtgcactccaccctgagggtgctcctccgcttgtaagatgatcttg 120

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Sbjct: 1381 tgggaagaaaaataaaatttccttcaggttttataaa 1416

>gi|31342209|ref|NM\_175594.2| Rattus norvegicus IGF-II mRNA-binding protein 1 (Imp-1)  
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Score = 1950 bits (1014), Expect = 0.0  
Identities = 1352/1519 (89%), Gaps = 7/1519 (0%)  
Strand = Plus / Plus

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Sbjct: 457 aggagtccgaaaaatacagatccggaatattccacctcagctccgatgggaagtgtggat 516

Query: 168 agcctgctggctcagtatgggtacagtagagaactgtgagcaagtgaacaccgagagttag 227  
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Sbjct: 517 agccttctggcccagtagcggcacagtgggagaactgtgagcaagtgaacaccgagagttag 576

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Query: 468 cggctcctggtgcccacccagtatgtgggtgccattattggcaaggagggggccaccatc 527  
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Query: 588 gcagctgaaaaagccatcagtgtgcactccaccctgagggctgctcctccgcttgaag 647  
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Sbjct: 1837 atcatcggacatttctatgccagtcagatggcccagcggaagatccgagacatcctggct 1896

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Query: 1602 cca-gcccctccctgtccc 1619  
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Length = 2105

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Identities = 1352/1519 (89%), Gaps = 7/1519 (0%)  
Strand = Plus / Plus

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Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtga 227  
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Sbjct: 517 agccttctggcccagtagggcacagtggagaactgtgagcaagtgaacaccgagagtga 576

Query: 228 acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287  
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Sbjct: 577 acggcgggtggtcaacgtcacctactctaaccgggagcagaccaggcaagccatcatgaag 636

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Query: 348	atagcacagggacctgagaatgggcgccgagggggccttggctctcggggtcagccccgc	407
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Sbjct: 757	caggggtcacccggtagcagcaggggcgccagccaagcagcagcaggtggacatccctctc	816
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Query: 828	accctttacaaccctgagaggaccatcactgtgaagggggccatcgagaattggtgcagg	887
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Query: 888	gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatgtggctgccatg	947
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Query: 948	a----gc--tctcacctgatccctggcctgaacctggctgctgtaggtcttttcccagct	1001
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Query: 1002	tcatccagcgcagtcctccgcgcctcccagcagcgttactggggctgctccctatagctcc	1061
Sbjct: 1357	tcttctaagtgcggttcgcgcctcctcccagcagcgctcactggggctgctccctatggctcc	1416

Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagtgag 227

[illegible]



Sbjct: 1204 gagcttgcagtcccacctcatccctgggcttaacctggctgctgtaggtctcttcccagc 1263

Query: 1001 ttcattccagcgcagtcgcccgcctcccagcagcggttactggggctgctccctatagctc 1060  
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Sbjct: 1264 ttcattccagcgcgtgtccctcctcctcccagcagtgctactggggctgctccctatagctc 1323

Query: 1061 ctttatgcaggctcccgagcaggagatgggtgcaggtgtttatccccgcccaggcagtgagg 1120  
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Sbjct: 1324 cttcatgcaggctccggagcaggagatgggtacaagtgttcatccccgcccaggctgtggg 1383

Query: 1121 cgccatcatcggaagaaggggcagcacatcaaacagctctcccggtt-gccagcgcct 1179  
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Sbjct: 1384 cgccatcattggcaagaagggccagcacatcaaacaactctcccg-tttcgccagcgcct 1442

Query: 1180 ccatcaagattgcaccacccgaaacacctgactccaaagttcgtatgggtatcatcactg 1239  
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Sbjct: 1443 ccatcaagattgctccaccagaaacacctgactccaaagttcgaatggtcgtcatcactg 1502

Query: 1240 gaccgccagaggcccaattcaaggctcaggggaagaatctatggcaaactcaaggaggaga 1299  
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Sbjct: 1503 gacccccagaggctcagttcaaggctcaggggaagaatttatggcaaactaaaagaagaga 1562

Query: 1300 acttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgccagcatcag 1359  
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Sbjct: 1563 atttctttggtcccaaggaggaagtaaagctagagaccacatacgggttccggcttcag 1622

Query: 1360 cagctggccgggtcattggcaaagggtggaaaaacgggtgaacgagttgcagaatttgacgg 1419  
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Query: 1420 cagctgaggtggttagtaccagagaccagacccctgatgagaacgaccaggtcatcgtga 1479  
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Query: 1480 aaatcatcggaacatttctatgccagtcagatgggtcaacggaagatccgagacatcctgg 1539  
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Query: 1540 cccagggttaagcagcagcatcagaagggaacagagtaaccaggcccaggcacggaggaagt 1599  
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Sbjct: 1803 ctcaagtttaagcaacagcaccagaagggaacagagcaacctggcccaggctcggaggaagt 1862

Query: 1600 gacca-gcccc-tccctgtccc 1619  
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Sbjct: 1863 gacccccgccccctcc-tgtccc 1883

>gi|31560605|ref|NM\_009951.2| Mus musculus insulin-like growth factor 2, binding pro  
(Igf2bp1), mRNA  
Length = 2780

Score = 1886 bits (981), Expect = 0.0  
Identities = 1343/1521 (88%), Gaps = 11/1521 (0%)  
Strand = Plus / Plus

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Query: 168 agcctgctggctcagtatggtacagtagagaactgtgagcaagtgaacaccgagagttag 227  
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Query: 228 acggcagtggtgaatgtcacctattccaaccgggagcagaccagggaagccatcatgaag 287  
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Query: 348 atagcacagggacctgagaatgggcgcgagggggctttggctctcggggctagcccc-g 406  
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Query: 407 ccagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccct 466  
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Query: 467 tcggctcctggtgcccaccagtagtggtgacctattggcaaggagggggccaccat 526  
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Query: 527 ccgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaaggagaacgcagg 586  
Sbjct: 932 ccgaaacatcacaaaacagacgcagtcgaagatagacgtgcataggaaggagaatgcggg 991

Query: 587 tgcagctgaaaaagccatcagtggtgactccaccctgagggctgctcctccgcttgtaa 646  
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Query: 647 gatgatcttgagattatgcataaaggagctaaggacacccaaacggctgacgaggttcc 706  
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Query: 1241 accgccagaggcccaattcaaggctcaggggaagaatctatggcaaactcaaggaggagaa 1300  
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Query: 1301 cttctttggtcccaaggaggaagtgaagctggagacccacatacgtgtgccagcatcagc 1360  
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Query: 1361 agctggccgggtcattggcaaagggtgaaaaacgggtgaacgagttgcagaatttgacggc 1420  
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Sbjct: 1772 agccggccgtgtcatcggaagggcggcaaacgggtgaatgagctgcagaacttgaccgc 1831

Query: 1421 agctgaggtggttagtaccagagaccagacccctgatgagaacgaccaggtcatcgtgaa 1480  
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Sbjct: 1832 agctgaggtggttagtgccaagagaccagaccccggtatgagaacgaccaagtcatgttaa 1891

Query: 1481 aatcatcggacatttctatgccagtcagatgggtcaacggaagatccgagacatcctggc 1540  
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Query: 1541 ccagggttaagcagcagcatcagaagggacagagtaaccagggccaggcacggaggaagtg 1600  
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Sbjct: 1952 tcaaggttaagcaacagcaccagaagggacagagcaacctggcccagggtcggaggaagtg 2011

Query: 1601 acca-gcccc-tccctgtccc 1619  
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Sbjct: 2012 accccgccccctcc-tgtccc 2031

>gi|12851513|dbj|AK013940.1| Mus musculus 13 days embryo head cDNA, RIKEN full-length library, clone:3110001D23 product:insulin-like growth factor 2, binding protein 1, full insert sequence  
Length = 2780

Score = 1886 bits (981), Expect = 0.0  
Identities = 1343/1521 (88%), Gaps = 11/1521 (0%)  
Strand = Plus / Plus

```
Query: 108  aggagccggaataattcaaatccgaaatattccaccccagctccgatgggaagtactggac 167
          ||||| ||||| || || || || || || || || || || || || || || || ||
Sbjct: 513  aggagtcggaataacagattcgcaatattccacctcagctccgatgggaagtgctagat 572

Query: 168  agcctgctggctcagtatggtagtagagaactgtgagcaagtgaacaccgagagttag 227
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 573  agcctgctggctcagtagcgttagtagagaactgtgagcaagtgaacactgaaagttag 632

Query: 228  acggcagtggtgaatgtcacctattccaaccgggagcagaccaggcaagccatcatgaag 287
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct: 633  acagctgtggtcaacgtcacctactctaaccgggagcagaccaggcaagctatcatgaag 692

Query: 288  ctgaatggccaccagttggagaacctgacctgaaggtctcctacatccccgatgagcag 347
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct: 693  ctaaatggccatcaactggagaacctgacctgaaggtctcctacatacctgatgagcag 752

Query: 348  atagcacaggacctgagaatgggcgccgagggggctttggctctcggggtcagcccc-g 406
          || | || || || || || || || || || || || || || || || || || || ||
Sbjct: 753  ataacgcaaggtcctgagaatgggcgctcgtggaggctttgggtctcggggccagccccgg 812

Query: 407  ccagggctcacctgtggcagcgggggccccagccaagcagcagcaagtggacatccccct 466
          | |||| || || || || || || || || || || || || || || || || || || ||
Sbjct: 813  caaggg-tcgcccgtggcagcaggggctccagccaagcagcagccagtggacatccctct 871

Query: 467  tcggctcctgggtgccaccagtagtggtggtccattattggcaaggagggggccaccat 526
          ||||| ||||| || || || || || || || || || || || || || || || || ||
Sbjct: 872  ccggctcctgggtgcctacgcagtagtaggcgtatcattggcaaggaggggtgccaccat 931

Query: 527  ccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaaggagaacgcagg 586
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 932  ccgaaacatcacaaaacagacgcagtcgaagatagacgtgcataggaaggagaatgcggg 991

Query: 587  tgcagctgaaaagccatcagtggtgactccaccctgagggtgctcctccgcttgtaa 646
          || || || || || || || || || || || || || || || || || || || || ||
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Query: 647  gatgatcttgagattatgcataaaggagtaaggacacaaaaacggctgacgaggttcc 706
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Sbjct: 1052 gatgatcttgagattatgcacaaggaggcaaaggacacaaaaacggcagatgaagttcc 1111

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Sbjct: 1112 cctgaagatcctggctcataacaacttcgtcgggcgactcattggcaaggaaggcgaa 1171
```

 **NCBI**  
Nucleotide   Protein   Translations   Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

The request ID is 1061911575-20294-2284897.BLASTQ3

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by  or select from: (none)

Expect value  range:

megablast seq ID NO: 6



Your request has been successfully submitted and put into the Blast Queue.

Query = (3412 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions  Alignments

Alignment view

Start formatting  
from query #

Limit results by  or select from:

Expect value  
range:

Results file ☐



# results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061911546-21269-1691103.BLASTQ3

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,886,208 sequences; 8,918,056,233 total letters

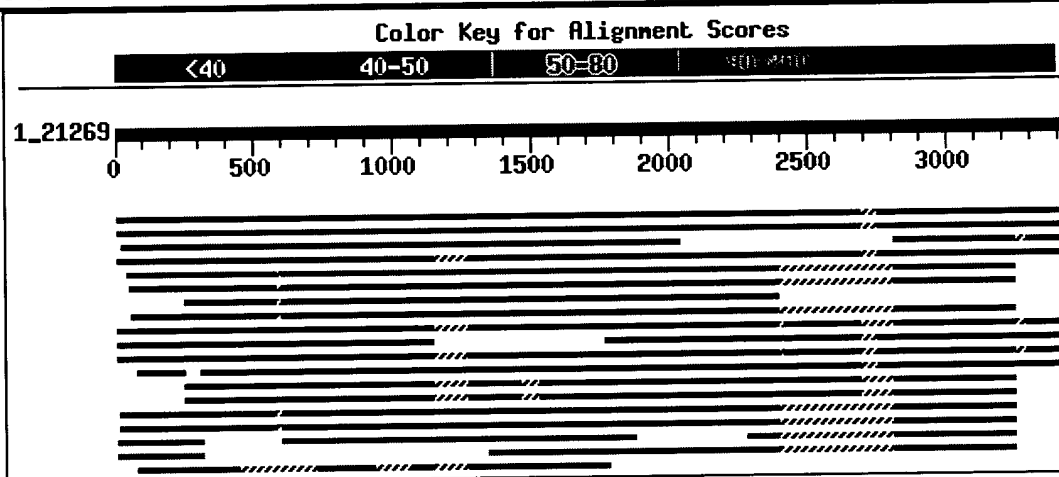
Taxonomy reports

Query=

(3412 letters)

## Distribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

gi 27552765 ref NM_006548.2	Homo sapiens IGF-II mRNA-bindin...	5107	0.0
gi 33878041 gb BC021290.2	Homo sapiens IGF-II mRNA-binding...	5105	0.0
gi 4191609 gb AF117107.1	AF117107 Homo sapiens IGF-II mRNA...	3826	0.0
gi 4883680 gb AF057352.1	AF057352 Homo sapiens hepatocellul...	2675	0.0
gi 23958572 gb BC023758.1	Mus musculus RIKEN cDNA C330012H...	2182	0.0
gi 26093366 dbj AK049196.1	Mus musculus ES cells cDNA, RIK...	2182	0.0
gi 26090647 dbj AK044984.1	Mus musculus 9.5 days embryo pa...	2177	0.0
gi 26097330 dbj AK077404.1	Mus musculus 6 days neonate hea...	2165	0.0
gi 7656675 gb AC020629.6	Homo sapiens 12q BAC RP11-76E16 (...)	1873	0.0
gi 27485839 ref XM_208686.1	Homo sapiens similar to hepato...	1865	0.0
gi 15552942 emb AL596177.4	Human DNA sequence from clone R...	1759	0.0
gi 27413166 gb AC016961.28	Homo sapiens 3 BAC RP11-394J21 ...	1708	0.0
gi 31873661 emb BX537583.1	HSM806243 Homo sapiens mRNA; cDN...	1708	0.0
gi 19849375 gb AC104980.5	Homo sapiens chromosome 8, clone...	1665	0.0
gi 17298202 dbj AP004290.2	Homo sapiens genomic DNA, chrom...	1659	0.0
gi 33942111 ref NM_183029.1	Mus musculus RIKEN cDNA C33001...	1240	0.0
gi 32451876 gb BC054552.1	Mus musculus cDNA clone MGC:6242...	1240	0.0

gi	27666189	ref	XM 221343.1	Rattus norvegicus similar to I...	1221	0.0
gi	28492961	ref	XM 193835.2	Mus musculus RIKEN cDNA C33001...	1175	0.0
gi	30148117	ref	XM 291469.2	Homo sapiens similar to hepato...	827	0.0
gi	18464262	gb	AC105413.3	Homo sapiens BAC clone RP11-64A1...	669	0.0
gi	23355671	gb	AC108670.10	Homo sapiens 3 BAC RP11-218A22 ...	479	e-131
gi	17737024	gb	AC009247.13	AC009247 Homo sapiens 3q27 BAC ...	479	e-131
gi	26082515	dbj	AK031773.1	Mus musculus 11 days embryo hea...	406	e-109
gi	27665993	ref	XM 221344.1	Rattus norvegicus similar to I...	302	3e-78

## Alignments

>gi|27552765|ref|NM\_006548.2| Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mR  
Length = 3642

Score = 5107 bits (2656), Expect = 0.0

Identities = 2671/2686 (99%)

Strand = Plus / Plus

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Sbjct: 9      gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaaga 68

Query: 65      gacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacc 124
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Sbjct: 69      gacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacc 128

Query: 125     tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 184
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Sbjct: 129     tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 188

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Query: 245     cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaaagc 304
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Query: 305     taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 364
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Sbjct: 309     taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 368

Query: 365     atggacttttggtcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 424
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Sbjct: 369     atggacttttggtcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 428

Query: 425     aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 484
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Query: 485     agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 544
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Sbjct: 489     agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 548

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```



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Query: 725 tcactaagcagaccagtcctccgggtagatatccatagaaaagagaactctggagctgcag 784  
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Sbjct: 729 tcactaagcagaccagtcctccgggtagatatccatagaaaagagaactctggagctgcag 788

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|||||

Sbjct: 789 agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattc 848

Query: 845 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 904  
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Sbjct: 849 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 908

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Identities = 609/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

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Query: 3408 tattt 3412
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>gi|33878041|gb|BC021290.2| Homo sapiens IGF-II mRNA-binding protein 2, mRNA (cDNA c  
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Length = 3633

Score = 5105 bits (2655), Expect = 0.0  
Identities = 2670/2685 (99%)  
Strand = Plus / Plus

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Query: 66     acggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacct 125
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Sbjct: 61     acggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacct 120
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Query: 126	ccggcagctctttggggacaggaagctgccccctggcgggacaggtcctgctgaagtccgg	185
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Sbjct: 181	ctacgccttcgtggactacccccgaccagaactgggccatccgcgccatcgagaccctctc	240
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Sbjct: 241	gggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct	300
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Strand = Plus / Plus

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Query: 80 agctttacatcgggaacctgagccccgccgtcaccgccgacgacctccggcagctctttg 139  
|||||  
Sbjct: 57 agctttacatcgggaacctgagccccgccgtcaccgccgacgacctccggcagctctttg 116

Query: 140 gggacaggaagctgcccctggcgggacaggtcctgctgaagtccggctacgccttcgtgg 199  
|||||  
Sbjct: 117 gggacaggaagctgcccctggcgggacaggtcctgctgaagtccggctacgccttcgtgg 176

Query: 200 actaccccgaccagaactgggccatccgcgccatcgagaccctctcgggtaaagtggaat 259  
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Sbjct: 177 actaccccgaccagaactgggccatccgcgccatcgagaccctctcgggtaaagtggaat 236

Query: 260 tgcattgggaaaatcatggaagttgattactcagtctctaaaaagctaaggagcaggaaaa 319  
|||||  
Sbjct: 237 tgcattgggaaaatcatggaagttgattactcagtctctaaaaagctaaggagcaggaaaa 296

Query: 320 ttcagattcgaaacatccctcctcacctgcagtgagggtgttgatggacttttggctc 379  
|||||  
Sbjct: 297 ttcagattcgaaacatccctcctcacctgcagtgagggtgttgatggacttttggctc 356

Query: 380 aatatgggacagtgaggaaatgtggaacaagtcaacacagacacagaaaccgccgttgtca 439  
|||||  
Sbjct: 357 aatatgggacagtgaggaaatgtggaacaagtcaacacagacacagaaaccgccgttgtca 416

Query: 440 acgtcacatatgcaacaagagaagaagcaaaaatagccatggagaagctaagcgggcatc 499

```

      |||
Sbjct: 417 acgtcacatatgcaacaagagaagaagcaaaaatagccatggagaagctaagcgggcatc 476

Query: 500 agtttgagaactactccttcaagatttcctacatcccggatgaagaggtgagctcccctt 559
      |||
Sbjct: 477 agtttgagaactactccttcaagatttcctacatcccggatgaagaggtgagctcccctt 536

Query: 560 cgccccctcagcgagcccagcgtggggaccactcttcccgggagcaaggccacgccccctg 619
      |||
Sbjct: 537 cgccccctcagcgagcccagcgtggggaccactcttcccgggagcaaggccacgccccctg 596

Query: 620 ggggcacttctcaggccagacagattgatttcccgctgcggatcctggtccccaccagt 679
      |||
Sbjct: 597 ggggcacttctcaggccagacagattgatttcccgctgcggatcctggtccccaccagt 656

Query: 680 ttgttggtgccatcatcggaaggagggttgaccataaagaacatcactaagcagaccc 739
      |||
Sbjct: 657 ttgttggtgccatcatcggaaggagggttgaccataaagaacatcactaagcagaccc 716

Query: 740 agtcccgggtagatatccatagaaaagagaactctggagctgcagagaagcctgtcacca 799
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Sbjct: 717 agtcccgggtagatatccatagaaaagagaactctggagctgcagagaagcctgtcacca 776

Query: 800 tccatgccaccccagaggggacttctgaagcatgccgcatgattcttgaaatcatgcaga 859
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Sbjct: 777 tccatgccaccccagaggggacttctgaagcatgccgcatgattcttgaaatcatgcaga 836

Query: 860 aagaggcagatgagaccaaactagccgaagagattcctctgaaaatcttggcacacaatg 919
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Sbjct: 837 aagaggcagatgagaccaaactagccgaagagattcctctgaaaatcttggcacacaatg 896

Query: 920 gcttggttgaagactgattggaaaagaaggcagaaatttgaagaaaattgaacatgaaa 979
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Sbjct: 897 gcttggttgaagactgattggaaaagaaggcagaaatttgaagaaaattgaacatgaaa 956

Query: 980 cagggaccaagataacaatctcatctttgcaggatttgagcatatacaacccggaaagaa 1039
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Sbjct: 957 cagggaccaagataacaatctcatctttgcaggatttgagcatatacaacccggaaagaa 1016

Query: 1040 ccatcactgtgaagggcacagttgaggcctgtgccagtgtgagatagagattatgaaga 1099
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Sbjct: 1017 ccatcactgtgaagggcacagttgaggcctgtgccagtgtgagatagagattatgaaga 1076

Query: 1100 agctgcgtgaggcctttgaaaatgatatgctggctgttaaccaacaagccaatctgatcc 1159
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Sbjct: 1077 agctgcgtgaggcctttgaaaatgatatgctggctgttaaccaacaagccaatctgatcc 1136

Query: 1160 caggggtgaacctcagcgcacttggcatcttttcaacaggactgtccgtgctatctccac 1219
      |||
Sbjct: 1137 caggggtgaacctcagcgcacttggcatcttttcaacaggactgtccgtgctatctccac 1196

Query: 1220 cagcagggccccgcggagctccccccgctgccccctaccaccccttcaactaccactccg 1279
```

Sbjct: 1197 cagcagggccccgcggagctcccccgctgccccctaccacccttcactaccactccg 1256

Query: 1280 gatacttctccagcctgtacccccatcaccagtttgcccgttcccgcacatcactctt 1339  
Sbjct: 1257 gatacttctccagcctgtacccccatcaccagtttgcccgttcccgcacatcactctt 1316

Query: 1340 atccagagcaggagattgtgaatctcttcacccaacccaggctgtggcgccatcatcg 1399  
Sbjct: 1317 atccagagcaggagattgtgaatctcttcacccaacccaggctgtggcgccatcatcg 1376

Query: 1400 ggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaagattg 1459  
Sbjct: 1377 ggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaagattg 1436

Query: 1460 cccctgcggaaggccagacgtcagcgaaaggatggtcatcatcaccgggccaccggaag 1519  
Sbjct: 1437 cccctgcggaaggccagacgtcagcgaaaggatggtcatcatcaccgggccaccggaag 1496

Query: 1520 cccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctttaacc 1579  
Sbjct: 1497 cccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctttaacc 1556

Query: 1580 ccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttcacagctggccggg 1639  
Sbjct: 1557 ccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttcacagctggccggg 1616

Query: 1640 tgattggcaaagggtggcaagaccgtgaacgaactgcagaacttaaccagtgcagaagtca 1699  
Sbjct: 1617 tgattggcaaagggtggcaagaccgtgaacgaactgcagaacttaaccagtgcagaagtca 1676

Query: 1700 tcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcagaattatcgggc 1759  
Sbjct: 1677 tcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtgatcgtcagaattatcgggc 1736

Query: 1760 acttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggtgaagc 1819  
Sbjct: 1737 acttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggtgaagc 1796

Query: 1820 agcaggagcagaaataccctcagggagtcgcctcacagcgcagcaagtgaggctcccaca 1879  
Sbjct: 1797 agcaggagcagaaataccctcagggagtcgcctcacagcgcagcaagtgaggctcccaca 1856

Query: 1880 ggcaccagcaaaaacaacggatgaatgtagccctccaacacctgacagaatgagacaaa 1939  
Sbjct: 1857 ggcaccagcaaaaacaacggatgaatgtagccctccaacacctgacagaatgagacaaa 1916

Query: 1940 cgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctgcggag 1999  
Sbjct: 1917 cgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctgcggag 1976

Query: 2000 gcggccagggactctgccgaggccctgagaaccc 2033

|||||  
Sbjct: 1977 gcggccagggactctgccgaggccctgagaaccc 2010

>gi|4883680|gb|AF057352.1|AF057352 Homo sapiens hepatocellular carcinoma autoantigen  
complete cds  
Length = 3667

Score = 2675 bits (1391), Expect = 0.0  
Identities = 1406/1421 (98%)  
Strand = Plus / Plus

Query: 1270 acccactccggatacttctccagcctgtacccccatcaccagtttgccccgttcccgcat 1329  
|||||  
Sbjct: 1507 acccactccggatacttctccagcctgtacccccatcaccagtttgccccgttcccgcat 1566

Query: 1330 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggc 1389  
|||||  
Sbjct: 1567 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggc 1626

Query: 1390 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1449  
|||||  
Sbjct: 1627 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1686

Query: 1450 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggg 1509  
|||||  
Sbjct: 1687 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggg 1746

Query: 1510 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1569  
|||||  
Sbjct: 1747 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1806

Query: 1570 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1629  
|||||  
Sbjct: 1807 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1866

Query: 1630 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1689  
|||||  
Sbjct: 1867 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1926

Query: 1690 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1749  
|||||  
Sbjct: 1927 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1986

Query: 1750 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1809  
|||||  
Sbjct: 1987 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 2046

Query: 1810 cagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 1869  
|||||  
Sbjct: 2047 cagggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 2106

Query: 1870 ggctcccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacacctgacagaa 1929  
|||||  
Sbjct: 2107 ggctcccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacacctgacagaa 2166

Query: 1930 tgagaccaaacgcagccagccagatcgggagcaaaccaagaccatctgaggaatgagaa 1989  
|||||  
Sbjct: 2167 tgagaccaaacgcagccagccagatcgggagcaaaccaagaccatctgaggaatgagaa 2226

Query: 1990 gtctgcggaggcggccagggactctgccgaggccctgagaaccccaggggccgaggaggg 2049  
|||||  
Sbjct: 2227 gtctgcggaggcggccagggactctgccgaggccctgagaaccccaggggccgaggaggg 2286

Query: 2050 gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggc 2109  
|||||  
Sbjct: 2287 gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgccccccagggc 2346

Query: 2110 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2169  
|||||  
Sbjct: 2347 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2406

Query: 2170 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2229  
|||||  
Sbjct: 2407 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2466

Query: 2230 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggaagatg 2289  
|||||  
Sbjct: 2467 accctttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggaagatg 2526

Query: 2290 ttaagatatgtggcctgtgggttacacagggcgctgcagcggtaatatattttagaaat 2349  
|||||  
Sbjct: 2527 ttaagatatgtggcctgtgggttacacagggcgctgcagcggtaatatattttagaaat 2586

Query: 2350 aatatatcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnn 2409  
|||||  
Sbjct: 2587 aatatatcaaataactcaactaactccaatttttaataattattaatttttttttcttt 2646

Query: 2410 nnaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2469  
|||||  
Sbjct: 2647 ttaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2706

Query: 2470 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaatctcgtcgga 2529  
|||||  
Sbjct: 2707 tgtagagaggagctttgaggccaccgcacaaaattcacccagagggaatctcgtcgga 2766

Query: 2530 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2589  
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Sbjct: 2767 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2826

Query: 2590 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccatttctctttgc 2649  
|||||  
Sbjct: 2827 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccatttctctttgc 2886

Query: 2650 ttcacaggttttaactgggtttttgcatactgctatataa 2690  
|||||  
Sbjct: 2887 ttcacaggttttaactgggtttttgcatactgctatataa 2927

Score = 2182 bits (1135), Expect = 0.0

Identities = 1135/1135 (100%)

Strand = Plus / Plus

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Query: 6      cggaggaggcgaggagcgccgggtaccgggcccggggagccgcccgggctctcggggaagag 65
             |||
Sbjct: 372    cggaggaggcgaggagcgccgggtaccgggcccggggagccgcccgggctctcggggaagag 431

Query: 66     acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 125
             |||
Sbjct: 432    acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 491

Query: 126    ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 185
             |||
Sbjct: 492    ccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccgg 551

Query: 186    ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 245
             |||
Sbjct: 552    ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 611

Query: 246    gggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 305
             |||
Sbjct: 612    gggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 671

Query: 306    aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 365
             |||
Sbjct: 672    aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 731

Query: 366    tggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacaga 425
             |||
Sbjct: 732    tggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacaga 791

Query: 426    aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 485
             |||
Sbjct: 792    aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 851

Query: 486    gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 545
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Sbjct: 852    gctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaaga 911

Query: 546    ggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 605
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Sbjct: 912    ggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 971

Query: 606    aggccacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggtacct 665
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Sbjct: 972    aggccacgcccctgggggcacttctcaggccagacagattgatttcccgctgcggtacct 1031

Query: 666    ggtccccaccagtttggttgccatcatcggaaggagggttgaccataaagaacat 725
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Sbjct: 1032   ggtccccaccagtttggttgccatcatcggaaggagggttgaccataaagaacat 1091
```

```
Query: 726 cactaagcagaccagtcgccgggtagatatccatagaaaagagaactctggagctgcaga 785
          |||
Sbjct: 1092 cactaagcagaccagtcgccgggtagatatccatagaaaagagaactctggagctgcaga 1151

Query: 786 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 845
          |||
Sbjct: 1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 1211

Query: 846 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 905
          |||
Sbjct: 1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 1271

Query: 906 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 965
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Sbjct: 1272 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 1331

Query: 966 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1025
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Sbjct: 1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1391

Query: 1026 caaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1085
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Sbjct: 1392 caaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1451

Query: 1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1140
          |||
Sbjct: 1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1506

Score = 1052 bits (547), Expect = 0.0
Identities = 608/665 (91%), Gaps = 2/665 (0%)
Strand = Plus / Plus

Query: 2749 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2808
          |||
Sbjct: 2986 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgca-ccccccccc 3044

Query: 2809 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2868
          |||
Sbjct: 3045 ccaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2869 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 2928
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Sbjct: 3105 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtccta 3164

Query: 2929 gcgttttggaagaggaaaacaggaacccaccaaaccaatcaaccaacaaagaaaa 2988
          |||
Sbjct: 3165 gcgttttggaagaggaaaacaggaacccaccaaaccaatcaaccaacaaagaaaa 3224

Query: 2989 aattccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaata 3048
          |||
Sbjct: 3225 aattccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaata 3284
```

Query: 3049 ttcagcaaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 3107  
|||||  
Sbjct: 3285 ttcagcaaaatgattcctttcttttaaaaaaaaaaagtgaggaaagtagaaatttacc 3344

Query: 3108 aagggtgttggtggccaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3167  
|||||  
Sbjct: 3345 aagggtgttggtggccaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3404

Query: 3168 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3227  
|||||  
Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtttcccttagagatttt 3464

Query: 3228 gtaaagctgatagttggagcannnnnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3287  
|||||  
Sbjct: 3465 gtaaagctgatagttggagcattttttttatttttttaataaaaaatgagttggaaaaaaa 3524

Query: 3288 taagatatcaactgccagcctggagaagggtgacagtccaagtggtgcaacagctgttctga 3347  
|||||  
Sbjct: 3525 taagatatcaactgccagcctggagaagggtgacagtccaagtggtgcaacagctgttctga 3584

Query: 3348 attgtcttccgctagccaagaacnataatggccttcttttggacaaaccttgaaaatggt 3407  
|||||  
Sbjct: 3585 attgtcttccgctagccaagaacctataatggccttcttttggacaaaccttgaaaatggt 3644

Query: 3408 tatttt 3412  
|||||  
Sbjct: 3645 tatttt 3649

>gi|23958572|gb|BC023758.1| Mus musculus RIKEN cDNA C330012H03 gene, mRNA (cDNA clon  
IMAGE:5354659), partial cds  
Length = 3557

Score = 2182 bits (1135), Expect = 0.0  
Identities = 1607/1828 (87%), Gaps = 59/1828 (3%)  
Strand = Plus / Plus

Query: 596 cccgggagcaaggccac-gcccctgggggcatttctcaggccagacagattgatttcccg 654  
|||||  
Sbjct: 540 cccggaacaaggccacggccc-gggagctcttctcaggccagacagattgatttcccg 598

Query: 655 ctgcggatcctggtccccaccagtttgttggtgccatcatcgaaaggagggttgacc 714  
|||||  
Sbjct: 599 ctgcggatcctggtccccaccagtttgttggtgccatcatcgaaaggagggttgacc 658

Query: 715 ataaagaacatcactaagcagaccagtcgggtagatatccatagaaaagagaactct 774  
|||||  
Sbjct: 659 ataaagaacatcactaagcagaccagtcgggtagacatccacagaaaggagaactct 718

Query: 775 ggagctgcagagaagcctgtcaccatccatgccacccagaggggacttctgaagcatgc 834  
|||||  
Sbjct: 719 ggggctgcagagaagcctgtcacatccatgctacccagaaggacatctgaagcatgc 778



```

Query: 835      cgcatgattccttgaaatcatgcagaaaaggagcagatgagaccaaactagccgaagagatt 894
|||
Sbjct: 779      cgcatgattccttgagattatgcaaaaagaagctgatgagaccaaactggctgaggaggtt 838

Query: 895      cctctgaaaatcctggcacacaatggcttggttgaagactgattggaaaagaaggcaga 954
|||
Sbjct: 839      cctctgaaaatcctggcccacaatggcttcggttgaagactgattggcaaagaaggcaga 898

Query: 955      aatttgaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgcaggat 1014
||
Sbjct: 899      aacctgaagaaaatagaacatgagacagggaccaagataaacatctcatccttgcaggat 958

Query: 1015     ttgagcatataacaacccggaagaaccatcactgtgaagggca-cagttgaggcctgtgc 1073
|||
Sbjct: 959      ttgagcatttataaaccccgagagaaccatcacctgagggggcacca-ttgaagcctgtgc 1017

Query: 1074     cagtgtgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc 1133
||
Sbjct: 1018     caatgtgagatagagattatgaagaagctccgagaggcctttgagaacgacatgctggc 1077

Query: 1134     tgттаaccaacaagccaatctgatcccagggttgaaacctcagcgcacttggcatcttttc 1193
|||
Sbjct: 1078     cgттаaccaacaagccaatctgatcccagggttaaacctcagtgcacttggcatcttttc 1137

Query: 1194     aacaggactgtccgtgctat-ctccaccagcagggccccgcggagctcccccc-gctgcc 1251
||
Sbjct: 1138     gactggactgtctgtgct-tcctccaccagcagggccccggtggagttccccccag-t-cc 1194

Query: 1252     -ccctaccaccccttccactaccactccggatacttctccagcctgtacccccatcacca 1310
|||
Sbjct: 1195     tccctatcacccctttgctaccactccggatacttctccagctctgtaccctcatcacca 1254

Query: 1311     gttt-ggcccgttcccgcacatcatcactcttatccagagcaggagattgtgaa-tctcttc 1368
|||
Sbjct: 1255     -tttcggccccattcccacatcatcactcctaccagagcaggagactgt-aagtctcttc 1312

Query: 1369     atcccaaccaggtgtgtggcgccatcatcggaagaaggggggcacacatcaaacagctg 1428
|||
Sbjct: 1313     atcccaaccaggtgtgggtgctatcatcggaagaaggggggcacacatcaaacagctc 1372

Query: 1429     gcgagattcgccggagcctctatcaagattgccctgcggaaggcccagacgtcagcgaa 1488
||
Sbjct: 1373     gctcgatttgctggtgcctccatcaagattgctccagcagaagggtccagatgtcagtgag 1432

Query: 1489     aggatgggtcatcatcacccgggccaccggaagcccagttcaaggcccaggacggatcttt 1548
|||
Sbjct: 1433     aggatgggtcatcatcactggtcctcctgaagcccagtttaagggtcagggacggatcttt 1492

Query: 1549     gggaaactgaaagaggaaaacttctttaaccccaaagaagaagtgaagctggaagcgcat 1608
|||
Sbjct: 1493     gggaaactgaaggaagaaaacttctttaatcccaaagaagaagtgaagctggaggccac 1552

```

```
Query:   1609 atcagagtgccttcttcacagctggccggttgattggcaaaggaggcaagaccgtgaac 1668
          ||| |||| | |||| | || | || | |||| | || | || | |||| | || | |||
Sbjct:   1553 atccgagtcacctcgctcgaccgctggccggttgattggcaaggcgaggaaaaccgtgaac 1612

Query:   1669 gaactgcagaacttaaccagtgcagaagtcatcgtgcctcgtgaccaaaccgcatgaa 1728
          || | |||| | |||| | || | |||| | |||| | |||| | |||| | |||
Sbjct:   1613 gagctgcagaacttgacaagtgcagaagttatcgtgcctcgtgaccaaaccgcagacgag 1672

Query:   1729 aatgaggaagtgatcgtcagaattatcgggcacttctttgctagccagactgcacagcgc 1788
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1673 aatgaggaagtgatcgtcagaattatcgggcatttttttctagccagactgcacaacgc 1732

Query:   1789 aagatcagggaaattgtacaacaggtgaagcagcaggagcagaaataccctcagggagtc 1848
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1733 aagatcagggaaattgtacagcaggtgaagcagcaggagcagagataccctcagggagtc 1792

Query:   1849 gcctcacagcgcagcaagtgaggctcccacaggcaccagcaaacacggatgaatgtag 1908
          ||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1793 gccccacagcgcagcaagtgaggctcccacag-caccagcaag-caaccgatgaatgtag 1850

Query:   1909 ccctccaacacctgacagaatgagaccaaacgcagccagccagatcgggagcaaacc aa 1968
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1851 ccctccaacacctgacaga-tgagaccaaac--agccagc-agatcggaagcaaacc aa 1906

Query:   1969 agaccatct-gaggaatgagaagtctgcggaggcggccagggactctgccgaggcc-ctg 2026
          || | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1907 agagcatcccaggagtgcgagctctgcagag-cagccaggg-c-ctgcaga--cctct- 1960

Query:   2027 aga-accccagggg-ccgaggagggg-cggggaagggtcagccagggttg-ccagaaccac 2082
          | | | || | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   1961 acacatcct-gggatcc-aggagggcacagggaagg-c--c-aggtt-gtccagaaacac 2013

Query:   2083 cga--gccccgcctccc-gcc-cccagggttctgcaggctt--cagccatccacttca 2136
          || | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   2014 cgcttggcctgcc-cccagcttcccctgg-cttctgcaggcataacagccatccactgc- 2070

Query:   2137 ccatcca-ctcggtatctctcctaactcccacgacgctatcccttttagttgaactaaca 2195
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   2071 ccatccaactcagat-tctcctcagttcccaggacgctatccctttcggttgaactaaca 2129

Query:   2196 taggtgaacgtgttcaaagccaagcaaatgcac-acc-ttt-ttc-t-gtggcaaa-t 2249
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   2130 taggtgaacatgctcaaagccaagcaaatc-ctagccgttctttgttgtgg-aaagt 2187

Query:   2250 cgtctctgtacatgtgtgtacatatattagaaagggaag-atgttaagatatgtggcctgtg 2308
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   2188 tgtctctgtacatgtatgtacatatcagaaggggaaggatgttaagaaatgtggcctgtg 2247

Query:   2309 ggttacacaggggtgcctgcagcggtaatatatttttagaaataatatcaaataactcaa 2368
          |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||
Sbjct:   2248 ggttacacaggggtgcctgcagcgttaatataatttttagaaataatatcaaataactcaa 2307
```

```
Query: 2811 aggcaaagcagtgcctctgagtatcacatcacacaaaaggaacaaaagcgaaacacacaaa 2870
          |||||||
Sbjct: 2768 aggcaaagcagtgcctctgaatatcataccacacacaaggaacaaatgcgaaccacacaga 2827
```



Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions   Alignments

Alignment view

Limit results by  or select from:    
entrez query

Expect value    
range:

 **NCBI**  
Nucleotide      Protein      Translations      Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1946 letters)

*megablast seq 7*

The request ID is

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment  in

Number of: Descriptions   Alignments

Alignment view

Start formatting  
from query #

Limit results by  or select from:

Expect value    
range:

Results file ☐



# results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

SEQ 8

RID: 1061911967-29701-25492.BLASTQ3

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,886,208 sequences; 8,918,056,233 total letters

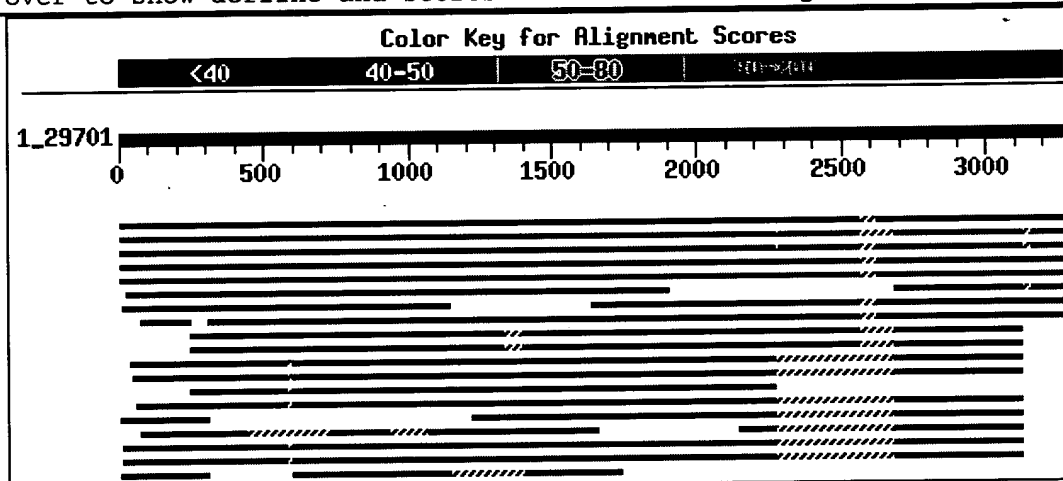
Taxonomy reports

Query=

(3283 letters)

## Distribution of 82 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

→	gi	4883680	gb	AF057352.1	AF057352	Homo sapiens hepatocellul...	4857	0.0
	gi	7656675	gb	AC020629.6		Homo sapiens 12q BAC RP11-76E16 (...)	3592	0.0
	gi	15552942	emb	AL596177.4		Human DNA sequence from clone R...	3505	0.0
→	gi	27552765	ref	NM_006548.2		Homo sapiens IGF-II mRNA-bind...	2675	0.0
	gi	33878041	gb	BC021290.2		Homo sapiens IGF-II mRNA-binding...	2675	0.0
→	gi	4191609	gb	AF117107.1	AF117107	Homo sapiens IGF-II mRNA...	2109	0.0
	gi	27485839	ref	XM_208686.1		Homo sapiens similar to hepato...	1865	0.0
	gi	27413166	gb	AC016961.28		Homo sapiens 3 BAC RP11-394J21 ...	1708	0.0
	gi	31873661	emb	BX537583.1	HSM806243	Homo sapiens mRNA; cDN...	1708	0.0
	gi	19849375	gb	AC104980.5		Homo sapiens chromosome 8, clone...	1665	0.0
	gi	17298202	dbj	AP004290.2		Homo sapiens genomic DNA, chrom...	1659	0.0
	gi	26093366	dbj	AK049196.1		Mus musculus ES cells cDNA, RIK...	1267	0.0
	gi	23958572	gb	BC023758.1		Mus musculus RIKEN cDNA C330012H...	1261	0.0
	gi	26090647	dbj	AK044984.1		Mus musculus 9.5 days embryo pa...	1256	0.0
	gi	26097330	dbj	AK077404.1		Mus musculus 6 days neonate hea...	1248	0.0
	gi	28492961	ref	XM_193835.2		Mus musculus RIKEN cDNA C33001...	1175	0.0
	gi	30148117	ref	XM_291469.2		Homo sapiens similar to hepato...	962	0.0

gi	33942111	ref	NM 183029.1	Mus musculus RIKEN cDNA C33001...	954	0.0
gi	32451876	gb	BC054552.1	Mus musculus cDNA clone MGC:6242...	954	0.0
gi	27666189	ref	XM 221343.1	Rattus norvegicus similar to I...	740	0.0
gi	18464262	gb	AC105413.3	Homo sapiens BAC clone RP11-64A1...	669	0.0
gi	23355671	gb	AC108670.10	Homo sapiens 3 BAC RP11-218A22 ...	479	e-131
gi	17737024	gb	AC009247.13	AC009247 Homo sapiens 3q27 BAC ...	479	e-131
gi	26082515	dbj	AK031773.1	Mus musculus 11 days embryo hea...	406	e-109
gi	27665993	ref	XM 221344.1	Rattus norvegicus similar to I...	302	2e-78

## Alignments

>gi|4883680|gb|AF057352.1|AF057352 Homo sapiens hepatocellular carcinoma autoantigen  
complete cds  
Length = 3667

Score = 4857 bits (2526), Expect = 0.0  
Identities = 2541/2556 (99%)  
Strand = Plus / Plus

Query: 6 cggaggaggcgcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaagag 65  
|||||  
Sbjct: 372 cggaggaggcgcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaagag 431

Query: 66 acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 125  
|||||  
Sbjct: 432 acggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgacgacct 491

Query: 126 ccggcagctctttggggacaggaagctgcccctggcgggacaggtcctgctgaagtccgg 185  
|||||  
Sbjct: 492 ccggcagctctttggggacaggaagctgcccctggcgggacaggtcctgctgaagtccgg 551

Query: 186 ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 245  
|||||  
Sbjct: 552 ctacgccttcgtggactaccccgaccagaactgggccatccgcgccatcgagaccctctc 611

Query: 246 gggtaaaagtgaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 305  
|||||  
Sbjct: 612 gggtaaaagtgaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagct 671

Query: 306 aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 365  
|||||  
Sbjct: 672 aaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgga 731

Query: 366 tggacttttggctcaatatgggacagtggaagaatgtggaacaagtcaacacagacacaga 425  
|||||  
Sbjct: 732 tggacttttggctcaatatgggacagtggaagaatgtggaacaagtcaacacagacacaga 791

Query: 426 aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 485  
|||||  
Sbjct: 792 aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggagaa 851

Query: 486 gctaagcgggcatcagtttgagaactactccttcaagatttctacatcccggatgaaga 545  
|||||  
Sbjct: 852 gctaagcgggcatcagtttgagaactactccttcaagatttctacatcccggatgaaga 911

Query: 546 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 605  
|||||  
Sbjct: 912 ggtgagctcccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagca 971

Query: 606 aggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcggatcct 665  
|||||  
Sbjct: 972 aggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcggatcct 1031

Query: 666 ggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaagaacat 725  
|||||  
Sbjct: 1032 ggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaagaacat 1091

Query: 726 cactaagcagaccagtcgggtagatatccatagaaaagagaactctggagctgcaga 785  
|||||  
Sbjct: 1092 cactaagcagaccagtcgggtagatatccatagaaaagagaactctggagctgcaga 1151

Query: 786 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 845  
|||||  
Sbjct: 1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcatgattct 1211

Query: 846 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 905  
|||||  
Sbjct: 1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaat 1271

Query: 906 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 965  
|||||  
Sbjct: 1272 cttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaatttgaagaa 1331

Query: 966 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1025  
|||||  
Sbjct: 1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatata 1391

Query: 1026 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1085  
|||||  
Sbjct: 1392 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgagat 1451

Query: 1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaacaccca 1145  
|||||  
Sbjct: 1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaacaccca 1511

Query: 1146 ctccggatacttctccagcctgtacccccatcaccagtttgggccgttcccgcacatca 1205  
|||||  
Sbjct: 1512 ctccggatacttctccagcctgtacccccatcaccagtttgggccgttcccgcacatca 1571

Query: 1206 ctcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggcgcat 1265  
|||||  
Sbjct: 1572 ctcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtgggcgcat 1631

Query: 1266 catcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaa 1325  
|||||  
Sbjct: 1632 catcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctctatcaa 1691



Query: 1326 gattgccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggggccacc 1385  
|||||  
Sbjct: 1692 gattgccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcaccggggccacc 1751

Query: 1386 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctt 1445  
|||||  
Sbjct: 1752 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaacttctt 1811

Query: 1446 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccacagctgg 1505  
|||||  
Sbjct: 1812 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccacagctgg 1871

Query: 1506 ccgggtgattggcaaagggtggcaagaccgtgaacgaactgcagaacttaaccagtgcaga 1565  
|||||  
Sbjct: 1872 ccgggtgattggcaaagggtggcaagaccgtgaacgaactgcagaacttaaccagtgcaga 1931

Query: 1566 agtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcagaattat 1625  
|||||  
Sbjct: 1932 agtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcagaattat 1991

Query: 1626 cgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggt 1685  
|||||  
Sbjct: 1992 cgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaacaggt 2051

Query: 1686 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtgaggctc 1745  
|||||  
Sbjct: 2052 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtgaggctc 2111

Query: 1746 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaatgaga 1805  
|||||  
Sbjct: 2112 ccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaatgaga 2171

Query: 1806 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctg 1865  
|||||  
Sbjct: 2172 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgaggaatgagaagtctg 2231

Query: 1866 cggaggcgccagggaactctgccgaggccctgagaacccaggggccgaggagggcggg 1925  
|||||  
Sbjct: 2232 cggaggcgccagggaactctgccgaggccctgagaacccaggggccgaggagggcggg 2291

Query: 1926 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcacccagggcttctg 1985  
|||||  
Sbjct: 2292 gaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcacccagggcttctg 2351

Query: 1986 caggcttcagccatccacttcaccatccactcggatctctcctgaactcccacgacgcta 2045  
|||||  
Sbjct: 2352 caggcttcagccatccacttcaccatccactcggatctctcctgaactcccacgacgcta 2411

Query: 2046 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcacaccct 2105  
|||||  
Sbjct: 2412 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcacaccct 2471

Query: 2106 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaaggaagatgttaag 2165  
|||||  
Sbjct: 2472 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaaggaagatgttaag 2531

Query: 2166 atatgtggcctgtgggttacacaggggtgcctgcagcggtaatatattttagaaataatat 2225  
|||||  
Sbjct: 2532 atatgtggcctgtgggttacacaggggtgcctgcagcggtaatatattttagaaataatat 2591

Query: 2226 atcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnnnaaa 2285  
|||||  
Sbjct: 2592 atcaaataactcaactaactccaatttttaataattattaatttttttttctttttaaa 2651

Query: 2286 gagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacggtgtag 2345  
|||||  
Sbjct: 2652 gagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacggtgtag 2711

Query: 2346 agaggagctttgaggccacccgcacaaaattcacccagagggaaatctcgctcggaaggac 2405  
|||||  
Sbjct: 2712 agaggagctttgaggccacccgcacaaaattcacccagagggaaatctcgctcggaaggac 2771

Query: 2406 actcacggcagttctggatcacctgtgtatgtcaacagaagggataccgtctccttgaag 2465  
|||||  
Sbjct: 2772 actcacggcagttctggatcacctgtgtatgtcaacagaagggataccgtctccttgaag 2831

Query: 2466 aggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgcttcac 2525  
|||||  
Sbjct: 2832 aggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgcttcac 2891

Query: 2526 aggttttaactgggtttttgcatactgctatataa 2561  
|||||  
Sbjct: 2892 aggttttaactgggtttttgcatactgctatataa 2927

Score = 1052 bits (547), Expect = 0.0  
Identities = 608/665 (91%), Gaps = 2/665 (0%)  
Strand = Plus / Plus

Query: 2620 cattcttttgaatttctcatccctccatctcaatcccgtatctacgcannnnnnnnnnnn 2679  
|||||  
Sbjct: 2986 cattcttttgaatttctcatccctccatctcaatcccgtatctacgcaccccccccccc 3045

Query: 2680 nnaggcaaagcagtgctctgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739  
|||||  
Sbjct: 3046 c-aggcaaagcagtgctctgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2740 aaccagcctcaacttacacttggttactcaaaagaacaagagtcattgggtacttgctcta 2799  
|||||  
Sbjct: 3105 aaccagcctcaacttacacttggttactcaaaagaacaagagtcattgggtacttgctcta 3164

Query: 2800 gcgttttggaagaggaaaacaggaacccaccaaaccaatcaaccaacaaagaaaa 2859  
|||||  
Sbjct: 3165 gcgttttggaagaggaaaacaggaacccaccaaaccaatcaaccaacaaagaaaa 3224

Query: 2860 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 2919  
|||||  
Sbjct: 3225 aattccacaatgaaagaatgtattttgtctttttgcattttggtgtataagccatcaata 3284

Query: 2920 ttcagcaaaatgattcctttctttnnnnnnnnnn-tgtggaggaaagtagaaatttacc 2978  
|||||  
Sbjct: 3285 ttcagcaaaatgattcctttctttaaaaaaaaaaagtgtggaggaaagtagaaatttacc 3344

Query: 2979 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038  
|||||  
Sbjct: 3345 aaggttggtggcccgaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3404

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3098  
|||||  
Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtttcccttagagatttt 3464

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158  
|||||  
Sbjct: 3465 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3524

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 3218  
|||||  
Sbjct: 3525 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 3584

Query: 3219 attgtcttcgctagccaagaacnataatggccttcttttgacaaaccttgaaaatgtt 3278  
|||||  
Sbjct: 3585 attgtcttcgctagccaagaacctataatggccttcttttgacaaaccttgaaaatgtt 3644

Query: 3279 tattt 3283  
|||||  
Sbjct: 3645 tattt 3649

>gi|7656675|gb|AC020629.6| Homo sapiens 12q BAC RP11-76E16 (Roswell Park Cancer Inst  
Library) complete sequence  
Length = 142971

Score = 3592 bits (1868), Expect = 0.0  
Identities = 2140/2268 (94%), Gaps = 31/2268 (1%)  
Strand = Plus / Plus

Query: 1 ggcagcggaggaggcgaggagcgccgggtaccgggcccggggagccgcccgtctcgggg 60  
|||||  
Sbjct: 132954 ggcagcagaggaggcgaggagcgagggtatcggg-cgggggagccgcccgtcgggg 133012

Query: 61 aagagacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgac 120  
||  
Sbjct: 133013 aacagacggatgatgaacaagctttacatcggaacctgagccccgccgtcaccgccgaa 133072

Query: 121 gacctccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaag 180  
|||||  
Sbjct: 133073 gacctccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctcaag 133132

Query: 181 tccggctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagacc 240  
|||

Sbjct: 133133 tcccgctacgccttcgtggactaccccgaccagaactgggccatccgcaccatcgagacc 133192

Query: 241 ctctcgggttaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctctaaa 300  
|||||  
Sbjct: 133193 ctctcgggtcaagtggaattgcatgggaaaatcatggaagttgattattcagtctctata 133252

Query: 301 aagctaaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtg 360  
|||||  
Sbjct: 133253 aagctaaggagcaggaaacattccgattcgaaatatccctcctcacctgcagtgggaggtg 133312

Query: 361 ttggatggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagac 420  
|||||  
Sbjct: 133313 ttggatggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagac 133372

Query: 421 acagaaaccgcccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatg 480  
|||||  
Sbjct: 133373 acagagaccgctgttgtcaacgtcacatatgcaacaaaagaagaagtaaaaatagccatg 133432

Query: 481 gagaagctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggat 540  
|||||  
Sbjct: 133433 aagaagctaagcgggcatcagtttgagaaccactacttcaagatttcctacatcccggat 133492

Query: 541 gaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgg 600  
|| |||||  
Sbjct: 133493 gacgaggtgagctgcccttcgccccctcagcgagcccagcgtggggaccactcttccctgg 133552

Query: 601 gagcaaggccacgcccctgggggcacttctcaggccagacagattgatttcccgtgcg- 659  
|||||  
Sbjct: 133553 gagcaaggccaagcccctgggggctcttctcaggccagacagattgatttcccactgcgt 133612

Query: 660 gatcctgggtccccaccagtttggttggtgccatcatcggaaggagggttgaccataaa 719  
| |||||  
Sbjct: 133613 g-tcctgttccccaccagtttggttggtgccatcatcggaaggagggttgaccataaa 133671

Query: 720 gaacatcactaagcagaccagtcgccgggtagatatccatagaaaagagaactctggagc 779  
|||||  
Sbjct: 133672 gaacatcactaagcagagccggtcgccgggtagacatctatagacaagagaactccagagc 133731

Query: 780 tgcagagaagcctgtcaccatccatgccaccccagaggggacttctgaagcatgccgcat 839  
|||||  
Sbjct: 133732 tgcagagaagcctgt---ca-ccatgccaccccagaggggacttctgaagcatgccgcat 133787

Query: 840 gattcttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctct 899  
|||||  
Sbjct: 133788 gattcttgaaataatgcagaaagaggcagatgaggccaaactagccgaagagattcctct 133847

Query: 900 gaaaatcttggcacacaatggcttggttggaagactgattggaaaagaaggcagaaattt 959  
|||||  
Sbjct: 133848 gaaaatcttggcccacaatggcttggttggaagactgattggaaaagaaggcagaaattt 133907

Query: 960 gaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgag 1019  
|||||

Sbjct: 133908 gaagaaaaatgaacatgaaacagggaccaagataacaatctcatcttcgcaggatttgag 133967

Query: 1020 catatacaacccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgc 1079  
|||||

Sbjct: 133968 catatacaacccggaagaaccatcactgtgaagggcacagtcgaggtctgtgccagtgc 134027

Query: 1080 tgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaa 1139  
|||||

Sbjct: 134028 tgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatacgctgactgttaa 134087

Query: 1140 caccactccggatacttctccagcctgtaccccatcaccagtttgcccgttcccga 1199  
|||||

Sbjct: 134088 taccacttcggatacttctccagcctgtaccccatcgccagtttgcccgttcccga 134147

Query: 1200 tcatcactcttatccagagcaggagattgtgaatctcttcatcccaaccaggctgtggg 1259  
|||||

Sbjct: 134148 tcatcactcttatccagagcaggagattgtcaatctcttcatcccaaccagggtgtggg 134207

Query: 1260 cgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctc 1319  
|||||

Sbjct: 134208 cgccatcatcggaagaagggggcacacatcaaacagctggcgagattcgtgggagcctc 134267

Query: 1320 tatcaagattgcccctgcggaaggcccagacgtcagcgaaaggatggatcatcatcacgg 1379  
|||||

Sbjct: 134268 catcaaga-t----c-gc-----ccctg-cgtcagc---ggaaggatcatcatcacctg 134310

Query: 1380 gccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaa 1439  
|||||

Sbjct: 134311 gccaccggaatcccagttcaaggcccaggacggatctttgggaaactgaaagaagaaaa 134370

Query: 1440 cttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccac 1499  
|||||

Sbjct: 134371 cttctttaaccccaaagaagacgtgaagctggaaacccatatcagagtgcctcttccac 134430

Query: 1500 agctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccag 1559  
|||||

Sbjct: 134431 cgctggccgggtgattggcaaagggggcaagaccgtgaatgaactgcagaatttaaccag 134490

Query: 1560 tgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcag 1619  
|||||

Sbjct: 134491 tgcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaaatgatcgtcag 134550

Query: 1620 aattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtaca 1679  
|||||

Sbjct: 134551 aattatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtaca 134610

Query: 1680 acaggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtg 1739  
|||||

Sbjct: 134611 acaggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtg 134670

Query: 1740 aggctcccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacaga 1799  
|||||

Sbjct: 134671 aggatccacaggcacaagcaaaacaacggaagaatgtagcccttccaacacctgacaga 134730

Query: 1800 atgagaccaaacgcagccagccagatcgggagcaaaccaagaccatctgaggaatgaga 1859  
|||||

Sbjct: 134731 atgagaccaaacacagccagccagatcaagagcaaaccaagaccatctgaggaatgaga 134790

Query: 1860 agtctgaggaggcgccagggactctgccgaggccctgagaacccaggggcccaggagg 1919  
|||||

Sbjct: 134791 agtctgaggaggcgccagggactctgtagaggccctgagaacccaggggcccaggagg 134850

Query: 1920 ggcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccgcacccagg 1979  
|||

Sbjct: 134851 ggtggggaaggtaaaccaggtttgccagaaccaccgggccccctcctcctgtccccagg 134910

Query: 1980 cttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacg 2039  
|||||

Sbjct: 134911 cttctgcaggcttcagccatccacttcaccatccactcggatctctccttaactcccacg 134970

Query: 2040 acgctatcccttttagttgaactaacataggtgaacgt-gttcaaagccaagcaaaatgc 2098  
|||||

Sbjct: 134971 acgctatcccttttagttgaactaaaataggtgaacattgttcaaagccaagcaaaatgc 135030

Query: 2099 acacccttttctgtggcaaatcgtctctgtacatgtgtgtacatattagaaaggggaaga 2158  
|||

Sbjct: 135031 acgccctttt-tgtggcaaatagtctctctacacgtgtatacatattagaaggggaaga 135089

Query: 2159 tgттаagatatgtggcctgtgggttacacagggcgctgcagcggtaatatatttttagaa 2218  
|||||

Sbjct: 135090 tgттаagatatgtggcctgtgggttacacagggcgctgcagcggtaatatatttttagaa 135149

Query: 2219 ataatatatcaaataactcaactaactccaatttttaataattatta 2266  
|||||

Sbjct: 135150 ataatatatcaaataact-aact--c-c-aatttttaataattatta 135192

Score = 675 bits (351), Expect = 0.0

Identities = 407/442 (92%), Gaps = 6/442 (1%)

Strand = Plus / Plus

Query: 2682 aggcaaagcagtgtctctgagtatcacatcacacaaaaggaacaaaagcgaaacacacaaa 2741  
|||||

Sbjct: 135606 aggcaaagcagtgtctctgagtatcacatcacacaaaaggaacaaaagcgaaacacacaaa 135665

Query: 2742 ccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtcctagc 2801  
|||||

Sbjct: 135666 ccagcctcaacttacacttggttactcaaaagaacaagagtcaatgggtacttgtcctagc 135725

Query: 2802 gttttggaagaggaaaacaggaacccaccaaaccaacaaatcaaccaacaaagaaaaaa 2861  
|||||

Sbjct: 135726 attttggaagaggaaaacaggaacctatcaaaccaacaaatcaaccaacaaagaaaaaa 135785

Query: 2862 ttccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaatatt 2921  
|||||

Sbjct: 135786 ttccacaatgaaagaatgtatcttcttttgcattttggtgtataagccatcaatact 135845

Query: 2922 cagcaaaatgattcctttctttnnnnnnnnnnntgtggaggaaagtagaaattta-ccaa 2980  
||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135846 cagcaaaataatttctttcttt-aaaaaaaaaatgtggaggaaagtagaaatttatacaa 135904

Query: 2981 ggttggtggccaggcggttaa-ttcacagannnnnnnaacgagaaaaacacacag-aa 3038  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135905 ggttggtgaccaggcggttaaactt-acagattattttaacgagaaaaacacacagaaa 135963

Query: 3039 gaagctacctcaggtg-tttttacctcagcaccttgctcttggtttcccttagagattt 3097  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135964 aaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttacagattt 136023

Query: 3098 tgtaaagctgatagttggagca 3119  
||||| ||| ||||| |||||

Sbjct: 136024 tgtaaaactgacagttggagca 136045

Score = 412 bits (214), Expect = e-111  
Identities = 258/279 (92%), Gaps = 3/279 (1%)  
Strand = Plus / Plus

Query: 2283 aaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacggtg 2342  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135206 aaagagagagcaggcttttctagactttaag--t-ctttctttagaaggtctcacggtg 135262

Query: 2343 tagagaggagctttgaggccaccgcacaaaattcaccagagggaaatctcgtcggaag 2402  
||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135263 tagagaggaccttcgaggccaccgcacaaaattcaccagagggaaatctcgtcggaag 135322

Query: 2403 gacactcacggcagttctggatcacctgtgtatgtcaacagaagggtatccgtctccttg 2462  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135323 gacactcacgcagttctggatcacctatgtatgtcaacagaagggtatctgtctccttg 135382

Query: 2463 aagaggaaactctgtcactcctcatgcctgtctaggtcatacacccatttctctttgctt 2522  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135383 aaggggaaactctgtcactcctcatgcctgtctaggtcatacacccatttctctttgctt 135442

Query: 2523 cacagggttttaactgggtttttgcatactgctatataa 2561  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 135443 cacagggttttaactgggtttttgcatactgctatataa 135481

Score = 208 bits (108), Expect = 6e-50  
Identities = 117/122 (95%)  
Strand = Plus / Plus

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 3218  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 136085 taagatatcaactgccagcctggagaaggtgacagtcgaagtgtgcaacagctgttctga 136144

Query: 3219 attgtcttccgctagccaagaaccnatatggccttcttttggacaaaccttgaaaatggt 3278  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 136145 attgtcttctgctagccaagaacctatatgaccttcttttggacaaactttgaaaatgtt 136204

Query: 3279 ta 3280

||

Sbjct: 136205 ta 136206

>gi|15552942|emb|AL596177.4| Human DNA sequence from clone RP11-325P15 on chromosome  
sequence

Length = 91084

Score = 3505 bits (1823), Expect = 0.0

Identities = 2138/2284 (93%), Gaps = 45/2284 (1%)

Strand = Plus / Plus

Query: 1 ggcagcggaggagggcaggagcgccgggtaccgggcccgggggagccgcccgtctcgggg 60  
|||||  
Sbjct: 9381 ggcagcggaggagggcaggagcgccgggtaccaggcccggggaggcgcccgtcccgggg 9440

Query: 61 aagagacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgac 120  
|||||  
Sbjct: 9441 aagagacgggtgatgaacaatctttacatcgggaaaccttagccctgcggtcaccgccgac 9500

Query: 121 gacctccggcagctctttggggacaggaagctgcccctggcgggacaggtcctgctgaag 180  
|||||  
Sbjct: 9501 gacctctggcagctctttggggacaggaagctgccccccaccggacaggtcctgctcaag 9560

Query: 181 tccggctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagacc 240  
|||||  
Sbjct: 9561 tccggctatgccttcgtggactacccctacaagaactgggcatccgcgccatcgagacc 9620

Query: 241 ctctcgggtaaagtgggaattgcatgggaaaatcatggaagttgattactcagtctctaaa 300  
|||||  
Sbjct: 9621 ctctcgggtaaagtgggaattgcatgggaaaatcatggaagttgattactcagtctctaaa 9680

Query: 301 aagctaaggagcaggaaaaattcagattcgaaacatccctcctcacctgcagtgggaggtg 360  
|||||  
Sbjct: 9681 aagctaaggaggagaaaaattcagattcgaaacatccctcctcacctccagtgggaggtg 9740

Query: 361 ttggatggacttttggctcaatatgggacagtggagaatgtgg---aacaagtcaacaca 417  
|||||  
Sbjct: 9741 ttggatggacttttggctcaatatggaacagtggagaatgtggaacaacaagtcaacaca 9800

Query: 418 gacacagaaaccgcccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaaatagcc 477  
|||||  
Sbjct: 9801 gacacagaaaccactgttgtcaacgtcacatatgcaac-a-ag-agaag-aaaatagac 9855

Query: 478 atggagaagctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccg 537  
|||||  
Sbjct: 9856 atggagaggctaagcgggcatcagtttgagaactagtcccttcaagatttcctacatcccg 9915

Query: 538 gatgaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcc 597  
|||||  
Sbjct: 9916 gatgaagaggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcc 9975



Query: 598	c-gggagcaaggccacgcccctgggggcacttctcaggccagacagattgatttcccgcct	656
Sbjct: 9976	cggggagcaaggccacgaccctgggggcgcttcttaggccagacagattgatttccctgct	10035
Query: 657	gc-ggatccttggtcccc-ac-----ccagtttggttggtgccatcatcgaaaggagggct	709
Sbjct: 10036	gcagg-tcctggtcccctacagtttgagtttggttggtgccatcatcagaaaggagggct	10094
Query: 710	tgaccataaagaacatcactaagcagacccagtcgccggtagatatccatagaaaagaga	769
Sbjct: 10095	tgaccataaagaacatcactaagtagaccagtcgccgtagatatccatagaaaagaga	10154
Query: 770	actctggagctgcagagaagcctgtcaccatccatgccaccccagaggggacttctgaag	829
Sbjct: 10155	actctggagctgcagagaagcctgtcaccatccatgccaccccaggggggacttctgaag	10214
Query: 830	catgccgcatgattcttgaaatcatgcagaaagaggcagatgagacaaactagccgaag	889
Sbjct: 10215	catgcctcatgattcttgaaatcatgcagaaagaggcagatgagaacaaactagccgaag	10274
Query: 890	agattcctctgaaaatcttggcacacaatggccttggttggaagactgattggaaaagaag	949
Sbjct: 10275	agattcctctgaaaatcttggcccacaatggc-----tt---g---g-ttggaaaagaag	10322
Query: 950	gcagaaatttgaagaaaattgaacatgaaacagggaccaagataacaatctcatctttgc	1009
Sbjct: 10323	gcagaaatttgaagaaaattgaacatgaaacagggaccaagatagcaatctcatctttgc	10382
Query: 1010	aggatttgagcatatacaacccggaaagaaccatcactgtgaagggcacag-ttgaggcc	1068
Sbjct: 10383	aggatttgagcataaataaccaggaaagaatcatcactgtgaagggcacagtttgaggcc	10442
Query: 1069	tgtgccagtgtgagatagagattatgaagaagctgcgtgaggcctttgaaaatgatatg	1128
Sbjct: 10443	tgtgccagtgtgagatagagattatgaagaagctgcgtgagacctttgaaaatgatatg	10502
Query: 1129	ctggctgttaacacccactccgatacttctccagcctgtacccccatcaccagtttggc	1188
Sbjct: 10503	ttggctgttaataacgcactccgatacttctccagcctgtacccccatcaccaggttggc	10562
Query: 1189	ccgttcccgcacatcatcactcttatccagagcaggagattgtgaatctcttcatcccaacc	1248
Sbjct: 10563	ccgttcccgcacatcatcactcttatccagagcaggaggtgtgaatctcttcatcccaacc	10622
Query: 1249	caggctgtgggcgccatcatcggaagaagggg-gcacacatcaaacagctggcgagatt	1307
Sbjct: 10623	caggctgtgggcgccattatcaggaag-aggggagcacacatcaaacagctggcgagatt	10681
Query: 1308	cgccggagcctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggatgggt	1367
Sbjct: 10682	cgccacagcctccatcaagatcgccctgcggaaggcccagacgtcaacgaaaggatgggt	10741

Query: 1368 catcatcaccgggccaccggaagcccagttcaaggcccaggacggatctttgggaaact 1427  
|||||  
Sbjct: 10742 catcatcaccgggccaccggaagcccagttcaaggcccaggacggatctttgggaaact 10801

Query: 1428 gaaagaggaaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagt 1487  
|||||  
Sbjct: 10802 gaaagaagaaaacttctttaaccccaaagaagaagtgaagctggaagcccgtatcagagt 10861

Query: 1488 gccctcttcacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgca 1547  
|||||  
Sbjct: 10862 gccctcttcacagctggccgggtgattggcaaaggtgtcaataccttgaatgaactgca 10921

Query: 1548 gaacttaaccagtgcagaagtcctgcctcgtgaccaaaccgagatgaaaatgagga 1607  
|||||  
Sbjct: 10922 gaacttaaccagtgcagaagtcctgcctcgtgaccaaaggcagatgaaaatgagga 10981

Query: 1608 agtgatcgtcagaattatcgggcacttctttgcta-gccagactgcacagcgcaagatca 1666  
|||||  
Sbjct: 10982 agtgatcgtcagaattattggacacttctttgctaccca-actgcatagcacaagatca 11040

Query: 1667 gggaaattgtacaacaggtgaagcagcaggagcagaaataccctcaggagtcgcctcac 1726  
|||||  
Sbjct: 11041 gggaaactgtacaacaggtgaagcagcaagagcagaaataccctcaggagtcgcctcac 11100

Query: 1727 agcgcagcaagtgaggctccacaggcaccagcaaaacaacggatgaatgtagcccttcc 1786  
|||  
Sbjct: 11101 agcacagcaagtgaggctccacaggcaccagcaaaacaacggatgaatggagcccttcc 11160

Query: 1787 aacacctgacagaatgagaccaaacgcagccagccagatcgggagcaaaccaaagaccat 1846  
|||||  
Sbjct: 11161 aacacctgacagaatgagaccaaacacagccagccagatcgggagcaaaccaaagaccat 11220

Query: 1847 ctgaggaatgagaagtctgcgaggcgccaggactctgccgaggccctgagaaccca 1906  
|||||  
Sbjct: 11221 ctgaggaatgagaagtctgcgaggctgccagggactctgaagaggccctgagaattcca 11280

Query: 1907 ggggcccaggagggggcggggaaggtcagccaggttgcgagaaccaccgagccccgcctc 1966  
|||||  
Sbjct: 11281 ggggcccaggaggggtggggaaggtcagccaggttgcgagaaccactgggccc-gcttc 11339

Query: 1967 ccgcccc--cagggtctctgcaggcttcagccatccacttcaccatccactcggatctc 2024  
|||  
Sbjct: 11340 tcacccccatcagggtctctgcaggcttcagccatccacttcaccatccactccgatctc 11399

Query: 2025 tcctgaactcccacgacgctatcccttttagttgaactaacataggtgaacgtgttcaa 2084  
|||||  
Sbjct: 11400 tccttaactcccacgacgctatcccttttagttgaactaacatag-tgat-gcgttcaa 11457

Query: 2085 gccaaagcaaaatgcacaccctttttctgtggcaaactcgtctctgtacatgtgtgtacata 2144  
|||||  
Sbjct: 11458 gccaaagcaaaatgcacaccctttttctgtgacaagtcctctgtacatgtgtatacata 11517

```
Query: 3097  ttgtaaagctgatagttggagca 3119
             |||||
Sbjct: 12470  ttgtaaaactgatagttggagca 12492
```

Score = 437 bits (227), Expect = e-119  
Identities = 266/284 (93%), Gaps = 5/284 (1%)  
Strand = Plus / Plus

Query: 2283 aaagagaaagcaggccttttctagacttt-aaagaataaaag----tctttgggaggtctca 2337  
|||  
Sbjct: 11651 aaagagaaagcaggccttttctagacttttaaagaataaaagtctttctttgggaggtctca 11710

Query: 2338 cgggtgtagagaggagctttgagggcaccgcacaaaattcacccagagggaaatctcgtc 2397  
|||  
Sbjct: 11711 cagtatagacaggagctttgagggcaccgcacaaaattcacccagagggaaatctcaaa 11770

Query: 2398 ggaaggacactcacggcagttctggatcacctgtgtatgtcaacagaaggataccgtct 2457  
|||  
Sbjct: 11771 ggaaggacaatcacagcagttctggatcacctgtgtatgtcaacagaaggataccatct 11830

Query: 2458 ccttgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctt 2517  
|||  
Sbjct: 11831 ccttgaagaagaaactctgtcactcctcatgcctgtctagctcttacacccatttctctt 11890

Query: 2518 tgcttcacagggttttaaactgggtttttgcatactgctatataa 2561  
|||  
Sbjct: 11891 tgcttcacagggttttaaactggatttttgcatactgctatataa 11934

Score = 231 bits (120), Expect = 6e-57  
Identities = 123/125 (98%)  
Strand = Plus / Plus

Query: 3159 taagatatcaactgccagcctggagaagggtgacagtccaagtgtgcaacagctgttctga 3218  
|||  
Sbjct: 12533 taagatatcaactgccagcctggagaagggtgacagtccaagtgtgcaacagctgttctga 12592

Query: 3219 attgtcttccgctagccaagaacnataatggccttcttttggacaaaccttgaaaatgtt 3278  
|||  
Sbjct: 12593 attgtcttctgctagccaagaacctatattggccttcttttggacaaaccttgaaaatgtt 12652

Query: 3279 tatttt 3283  
|||  
Sbjct: 12653 tatttt 12657

>gi|27552765|ref|NM\_006548.2| Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mR  
Length = 3642

Score = 2675 bits (1391), Expect = 0.0  
Identities = 1406/1421 (98%)  
Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcaccagtttggcccgttcccgcat 1200  
|||  
Sbjct: 1274 acccactccggatacttctccagcctgtacccccatcaccagtttggcccgttcccgcat 1333

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1260  
|||

Sbjct: 1334 catcactcttatccagagcaggagattgtgaatctcttcatcccaacccaggctgtgggc 1393

Query: 1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1320  
|||||

Sbjct: 1394 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1453

Query: 1321 atcaagattgccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccggg 1380  
|||||

Sbjct: 1454 atcaagattgccctgcggaaggccagacgtcagcgaaaggatggatcatcatcaccggg 1513

Query: 1381 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1440  
|||||

Sbjct: 1514 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaac 1573

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1500  
|||||

Sbjct: 1574 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgcctcttccaca 1633

Query: 1501 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1560  
|||||

Sbjct: 1634 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1693

Query: 1561 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1620  
|||||

Sbjct: 1694 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1753

Query: 1621 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1680  
|||||

Sbjct: 1754 attatcgggcacttctttgctagccagactgcacagcgcaagatcagggaaattgtacaa 1813

Query: 1681 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 1740  
|||||

Sbjct: 1814 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagcgagcaagtga 1873

Query: 1741 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaa 1800  
|||||

Sbjct: 1874 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaacacctgacagaa 1933

Query: 1801 tgagaccaaaccgagccagccagatcgggagcaaaccagaccatctgaggaatgagaa 1860  
|||||

Sbjct: 1934 tgagaccaaaccgagccagccagatcgggagcaaaccagaccatctgaggaatgagaa 1993

Query: 1861 gtctgaggaggcgccaggactctgccgaggccctgagaaccccaggggcccaggaggg 1920  
|||||

Sbjct: 1994 gtctgaggaggcgccaggactctgccgaggccctgagaaccccaggggcccaggaggg 2053

Query: 1921 gcggggaagggtcagccaggtttgccagaaccaccgagccccgcctccgccccccagggc 1980  
|||||

Sbjct: 2054 gcggggaagggtcagccaggtttgccagaaccaccgagccccgcctccgccccccagggc 2113

Query: 1981 ttctgcaggcttcagccatccacttcaccatccactcggatctctcctgaactcccacga 2040  
|||||

Sbjct: 2114 ttctgcaggcttcagccatccacttcaccatccactcggatctctctctgaactcccacga 2173

Query: 2041 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2100  
|||||

Sbjct: 2174 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaagcaaaatgcac 2233

Query: 2101 accctttttctgtggcaaactcgtctctgtacatgtgtgtacatattagaaaggggaagatg 2160  
|||||

Sbjct: 2234 accctttttctgtggcaaactcgtctctgtacatgtgtgtacatattagaaaggggaagatg 2293

Query: 2161 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaaat 2220  
|||||

Sbjct: 2294 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatatatttttagaaat 2353

Query: 2221 aatatatcaaataactcaactaactccaatttttaataattattaannnnnnnnnnnnnn 2280  
|||||

Sbjct: 2354 aatatatcaaataactcaactaactccaatttttaataattattaatttttttttcttt 2413

Query: 2281 nnaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2340  
|||||

Sbjct: 2414 ttaagagaaagcaggcttttctagactttaagaataaagtctttgggaggtctcacgg 2473

Query: 2341 tgtagagaggagctttgaggccacccgcacaaaattcacccagagggaatctcgtcgg 2400  
|||||

Sbjct: 2474 tgtagagaggagctttgaggccacccgcacaaaattcacccagagggaatctcgtcgg 2533

Query: 2401 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2460  
|||||

Sbjct: 2534 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagggaataccgtctcct 2593

Query: 2461 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgc 2520  
|||||

Sbjct: 2594 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacacccatttctctttgc 2653

Query: 2521 ttcacaggttttaactgggtttttgcatactgctatataa 2561  
|||||

Sbjct: 2654 ttcacaggttttaactgggtttttgcatactgctatataa 2694

Score = 2184 bits (1136), Expect = 0.0  
Identities = 1136/1136 (100%)  
Strand = Plus / Plus

Query: 5 gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaaga 64  
|||||

Sbjct: 9 gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggctctcggggaaga 68

Query: 65 gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacc 124  
|||||

Sbjct: 69 gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcaccgccgacgacc 128

Query: 125 tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 184  
|||||

Sbjct: 129 tccggcagctctttggggacaggaagctgccctggcgggacaggtcctgctgaagtccg 188

Query: 185 gctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagaccctct 244  
|||||

Sbjct: 189 gctacgccttcgtggactaccccgaccagaactgggcatccgcgccatcgagaccctct 248

Query: 245 cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagc 304  
|||||

Sbjct: 249 cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagtctctaaaaagc 308

Query: 305 taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 364  
|||||

Sbjct: 309 taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtgggaggtgttgg 368

Query: 365 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 424  
|||||

Sbjct: 369 atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaacacagacacag 428

Query: 425 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 484  
|||||

Sbjct: 429 aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaatagccatggaga 488

Query: 485 agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 544  
|||||

Sbjct: 489 agctaagcgggcatcagtttgagaactactccttcaagatttcctacatcccggatgaag 548

Query: 545 aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagc 604  
|||||

Sbjct: 549 aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactcttcccgggagc 608

Query: 605 aagggcacgcccctgggggcacttctcaggccagacagattgatttcccgcgtgcggatcc 664  
|||||

Sbjct: 609 aagggcacgcccctgggggcacttctcaggccagacagattgatttcccgcgtgcggatcc 668

Query: 665 tgggtccccacccagtttgggtgggtgccatcatcgaaaggagggttgaccataaagaaca 724  
|||||

Sbjct: 669 tgggtccccacccagtttgggtgggtgccatcatcgaaaggagggttgaccataaagaaca 728

Query: 725 tcactaagcagaccagtcctcggttagatatccatagaaaagagaactctggagctgcag 784  
|||||

Sbjct: 729 tcactaagcagaccagtcctcggttagatatccatagaaaagagaactctggagctgcag 788

Query: 785 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatgccgcattgattc 844  
|||||

Sbjct: 789 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatgccgcattgattc 848

Query: 845 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 904  
|||||

Sbjct: 849 ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagattcctctgaaaa 908

Query: 905 tcttggcacacaatggcttgggttgggaagactgattggaaaagaaggcagaaatttgaaga 964  
|||||

Sbjct: 909 tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcagaaatttgaaga 968

Query: 965 aaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatat 1024  
|||||

Sbjct: 969 aaattgaacatgaaacagggaccaagataacaatctcatctttgcaggatttgagcatat 1028

Query: 1025 acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgaga 1084  
|||||

Sbjct: 1029 acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgccagtgtgaga 1088

Query: 1085 tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1140  
|||||

Sbjct: 1089 tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggctgttaac 1144

Score = 1058 bits (550), Expect = 0.0  
Identities = 609/665 (91%), Gaps = 2/665 (0%)  
Strand = Plus / Plus

Query: 2620 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnn 2679  
|||||

Sbjct: 2753 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgca-ccccccccc 2811

Query: 2680 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739  
|||||

Sbjct: 2812 ccaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2871

Query: 2740 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgtccta 2799  
|||||

Sbjct: 2872 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgtccta 2931

Query: 2800 gcgttttgaagaggaaaacaggaacccaccaaaccaaatcaaccaaacaaagaaaa 2859  
|||||

Sbjct: 2932 gcgttttgaagaggaaaacaggaacccaccaaaccaaatcaaccaaacaaagaaaa 2991

Query: 2860 aattccacaatgaaagaatgtattttgcattttggtgtataagccatcaata 2919  
|||||

Sbjct: 2992 aattccacaatgaaagaatgtattttgcattttggtgtataagccatcaata 3051

Query: 2920 ttcagcaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978  
|||||

Sbjct: 3052 ttcagcaaatgattcctttcttttaaaaaaaaaaattgtggaggaaagtagaaatttacc 3111

Query: 2979 aaggttggtggccagggcggttaattcacagannnnnnnaacgagaaaaacacacagaa 3038  
|||||

Sbjct: 3112 aaggttggtggccagggcggttaattcacagatttttttaacgagaaaaacacacagaa 3171

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgccttctgtgtttcccttagagatttt 3098  
|||||

Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgccttctgtgtttcccttagagatttt 3231

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158  
|||||



Sbjct: 3232 gtaaagctgatagttggagcattttttttatttttttaataaaaatgagttggaaaaaaaaa 3291

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218

|||||  
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3219 attgtcttccgctagccaagaaccnatatggccttcttttggacaaaccttgaaaatgtt 3278

|||||  
Sbjct: 3352 attgtcttccgctagccaagaacctatatggccttcttttggacaaaccttgaaaatgtt 3411

Query: 3279 tattt 3283

|||||  
Sbjct: 3412 tattt 3416

>gi|33878041|gb|BC021290.2| Homo sapiens IGF-II mRNA-binding protein 2, mRNA (cDNA c  
MGC:29539 IMAGE:5090334), complete cds  
Length = 3633

Score = 2675 bits (1391), Expect = 0.0

Identities = 1406/1421 (98%)

Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcaccagtttgcccggttcccgcat 1200

|||||  
Sbjct: 1265 acccactccggatacttctccagcctgtacccccatcaccagtttgcccggttcccgcat 1324

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1260

|||||  
Sbjct: 1325 catcactcttatccagagcaggagattgtgaatctcttcacccaaccaggctgtgggc 1384

Query: 1261 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1320

|||||  
Sbjct: 1385 gccatcatcgggaagaagggggcacacatcaaacagctggcgagattcgccggagcctct 1444

Query: 1321 atcaagattgcccctgcggaaggccagacgtcagcgaaaggatgggtcatcatcaccggg 1380

|||||  
Sbjct: 1445 atcaagattgcccctgcggaaggccagacgtcagcgaaaggatgggtcatcatcaccggg 1504

Query: 1381 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaaac 1440

|||||  
Sbjct: 1505 ccaccggaagcccagttcaaggcccaggacggatctttgggaaactgaaagaggaaaaac 1564

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgccctcttccaca 1500

|||||  
Sbjct: 1565 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgccctcttccaca 1624

Query: 1501 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1560

|||||  
Sbjct: 1625 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaacttaaccagt 1684

Query: 1561 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1620

|||||  
Sbjct: 1685 gcagaagtcacgtgcctcgtgaccaaaccgagatgaaaatgaggaagtgatcgtcaga 1744



Your request has been successfully submitted and put into the Blast Queue.

Query = (3283 letters)

The request ID is

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☐ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions  Alignments

Alignment view

Limit results by  or select from:

Expect value  range:



Your request has been successfully submitted and put into the Blast Queue.

seq

Query = (3283 letters)

The request ID is 1061911967-29701-25492.BLASTQ3

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML

Number of: Descriptions 100 Alignments 50

Alignment view Hit Table

Start formatting  
from query #

Limit results by  
entrez query or select from: (none)

Expect value  
range:

Results file ☐

# seq 5 vs patent database

Sequences producing significant alignments:

	Score (bits)	E Value	
gi 17910814 gb AR171864.1 AR171864 Sequence 5 from patent U...	3356	0.0	<i>parent instant</i>
gi 33019694 dbj BD209924.1  Isolated nucleic acid molecules...	3356	0.0	<i>instant</i>
<del>gi 33738475 gb AR343073.1 </del> Sequence 5 from patent US <u>6576756</u>	3356	0.0	<i>instant</i>
gi 17910816 gb AR171866.1 AR171866 Sequence 7 from patent U...	3285	0.0	
gi 33019696 dbj BD209926.1  Isolated nucleic acid molecules...	3285	0.0	
gi 33738477 gb AR343075.1  Sequence 7 from patent US 6576756	3285	0.0	
gi 23222756 dbj BD127811.1  Primer for synthesizing full-le...	2732	0.0	



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lcl|seq\_1 Length 1946 (1 .. 1946)

Sequence 2 gi 4191607 Length 2130 (1 .. 2130)



SEQ 7  
gi 4191607

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3484 bits (1812), Expect = 0.0  
 Identities = 1834/1845 (99%), Gaps = 6/1845 (0%)  
 Strand = Plus / Plus

```
Query:                108  aggagccggaaaattcaaatccgaaatattccaccccagctccgatggg
                        |||
Sbjct:                244  aggagccggaaaattcaaatccgaaatattccaccccagctccgatggg
IGF-II mRNA-binding protein 1 79  R S R K I Q I R N I P P Q L R W
```

```
Query:                168  agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaaca
                        |||
Sbjct:                304  agcctgctgggtcagtatggtacagtagagaactgtgagcaagtgaaca
IGF-II mRNA-binding protein 1 99  S L L A Q Y G T V E N C E Q V N
```

```
Query:                228  acggcagtggtgaatgtcacctattccaaccgggagcagaccagggaag
                        |||
Sbjct:                364  acggcagtggtgaatgtcacctattccaaccgggagcagaccagggaag
IGF-II mRNA-binding protein 1 119  T A V V N V T Y S N R E Q T R Q
```

```
Query:                288  ctgaatggccaccagttggagaaccatgccctgaaggtctcctacatcc
                        |||
Sbjct:                424  ctgaatggccaccagttggagaaccatgccctgaaggtctcctacatcc
IGF-II mRNA-binding protein 1 139  L N G H Q L E N H A L K V S Y I
```

Query:	348	atagcacagggacctgagaatgggcgccgagggggctttggctctcggg
Sbjct:	484	atagcacagggacctgagaatgggcgccgagggggctttggctctcggg
IGF-II mRNA-binding protein 1	159	I A Q G P E N G R R G G F G S R
Query:	408	cagggctcacctgtggcagcggggggccccagccaagcagcagcaagtgg
Sbjct:	544	cagggctcacctgtggcagcggggggccccagccaagcagcagcaagtgg
IGF-II mRNA-binding protein 1	179	Q G S P V A A G A P A K Q Q Q V
Query:	468	cggctcctgggtgcccacccagtatgtgggtgccattattggcaaggagg
Sbjct:	604	cggctcctgggtgcccacccagtatgtgggtgccattattggcaaggagg
IGF-II mRNA-binding protein 1	199	R L L V P T Q Y V G A I I G K E
Query:	528	cgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaagg
Sbjct:	664	cgcaacatcacaaaacagacccagtcgaagatagacgtgcataggaagg
IGF-II mRNA-binding protein 1	219	R N I T K Q T Q S K I D V H R K
Query:	588	gcagctgaaaaagccatcagtggtgcactccaccctgagggctgctcct
Sbjct:	724	gcagctgaaaaagccatcagtggtgcactccaccctgagggctgctcct
IGF-II mRNA-binding protein 1	239	A A E K A I S V H S T P E G C S
Query:	648	atgatccttgagattatgcataaagaggctaaggacacccaaaacggctg
Sbjct:	784	atgatccttgagattatgcataaagaggctaaggacacccaaaacggctg
IGF-II mRNA-binding protein 1	259	M I L E I M H K E A K D T K T A
Query:	708	ctgaagatcctggcccataataactttgtagggcgctctcattggcaagg
Sbjct:	844	ctgaagatcctggcccataataactttgtagggcgctctcattggcaagg
IGF-II mRNA-binding protein 1	279	L K I L A H N N F V G R L I G K
Query:	768	ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcgt
Sbjct:	904	ctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctcgt
IGF-II mRNA-binding protein 1	299	L K K V E Q D T E T K I T I S S
Query:	828	accctttacaaccctgagaggaccatcactgtgaagggggccatcgaga
Sbjct:	964	accctttacaaccctgagaggaccatcactgtgaagggggccatcgaga
IGF-II mRNA-binding protein 1	319	T L Y N P E R T I T V K G A I E
Query:	888	gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatg
Sbjct:	1024	gccgagcaggaaataatgaagaaagttcgggaggcctatgagaatgatg
IGF-II mRNA-binding protein 1	339	A E Q E I M K K V R E A Y E N D
Query:	948	agc-----tctcacctgatccctggcctgaacctggctgctgtaggtc
Sbjct:	1084	aqcctgcagctctcacctgatccctggcctgaacctggctgctgtaggtc

IGF-II mRNA-binding protein 1 359 S L Q S H L I P G L N L A A V G

Query: 1002 tcatccagcgcagtcctccgcccctccagcagcgttactggggctgctc  
|  
Sbjct: 1144 tcatccagcgcagtcctccgcccctccagcagcgttactggggctgctc  
IGF-II mRNA-binding protein 1 379 S S S A V P P P S S V T G A A

Query: 1062 tttatgcaggctcccgagcaggagatgggtgcagggtgtttatccccgccc  
|  
Sbjct: 1204 tttatgcaggctcccgagcaggagatgggtgcagggtgtttatccccgccc  
IGF-II mRNA-binding protein 1 399 F M Q A P E Q E M V Q V F I P A

Query: 1122 gccatcatcggaagaaggggcagcacatcaaacagctctccccggtttg  
|  
Sbjct: 1264 gccatcatcggaagaaggggcagcacatcaaacagctctccccggtttg  
IGF-II mRNA-binding protein 1 419 A I I G K K G Q H I K Q L S R F

Query: 1182 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggtta  
|  
Sbjct: 1324 atcaagattgcaccacccgaaacacctgactccaaagttcgtatggtta  
IGF-II mRNA-binding protein 1 439 I K I A P P E T P D S K V R M V

Query: 1242 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactca  
|  
Sbjct: 1384 ccgccagaggcccaattcaaggctcaggaagaatctatggcaaactca  
IGF-II mRNA-binding protein 1 459 P P E A Q F K A Q G R I Y G K L

Query: 1302 ttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgc  
|  
Sbjct: 1444 ttctttggtcccaaggaggaagtgaagctggagaccacatacgtgtgc  
IGF-II mRNA-binding protein 1 479 F F G P K E E V K L E T H I R V

Query: 1362 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcaga  
|  
Sbjct: 1504 gctggccgggtcattggcaaaggtggaaaaacggtgaacgagttgcaga  
IGF-II mRNA-binding protein 1 499 A G R V I G K G G K T V N E L Q

Query: 1422 gctgaggtggttagtaggaagagaccagaccctgatgagaacgaccagg  
|  
Sbjct: 1564 gctgaggtggttagtaggaagagaccagaccctgatgagaacgaccagg  
IGF-II mRNA-binding protein 1 519 A E V V V P R D Q T P D E N D Q

Query: 1482 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgag  
|  
Sbjct: 1624 atcatcggacatttctatgccagtcagatgggtcaacggaagatccgag  
IGF-II mRNA-binding protein 1 539 I I G H F Y A S Q M A Q R K I R

Query: 1542 caggttaagcagcagcatcagaagggacagagtaaccaggccagggcac  
|  
Sbjct: 1684 caggttaagcagcagcatcagaagggacagagtaaccaggccagggcac  
IGF-II mRNA-binding protein 1 559 Q V K Q Q H Q K G Q S N Q A Q A

Query: 1602 ccagcccctccctgtcccttngagtccaggacaacaacgggcagaaatc  
|

```
Sbjct:          1744 ccagccctccctgtcccttcgagtcaggacaacaacgggcagaaatc

Query:          1662 ctccccggcaggcctgagaatgagtgggaatccgggacacntgggccgg
                  |||
Sbjct:          1804 ctccccggcaggcctgagaatgagtgggaatccgggacacctgggccgg

Query:          1722 ggtttgccacttgattgagaaagatgttcagtgaggaaccctgatct
                  |||
Sbjct:          1864 ggtttgccacttgattgagaaagatgttcagtgaggaaccctgatct

Query:          1782 acacccacccaattggcccaacactgtntgccctcgggggtgtcagaaa
                  |||
Sbjct:          1924 acacccacccaattggcccaacactgtctgccctcgggggtgtcagaaa

Query:          1842 ggcacttttaaacgtggattgtttaagaagctctccaggccccaccaa
                  |||
Sbjct:          1984 ggcacttttaaacgtggattgtttaagaagctctccaggccccaccaa

Query:          1902 acacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 194
                  |||
Sbjct:          2044 acacctcagtggggaagaaaaataaaatttccttcagggttttaaaa 208
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 13  
Number of Sequences: 0  
Number of extensions: 13  
Number of successful extensions: 2  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 1946  
length of database: 8,918,056,233  
effective HSP length: 25  
effective length of query: 1921  
effective length of database: 8,918,056,208  
effective search space: 17131585975568  
effective search space used: 17131585975568  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)





# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

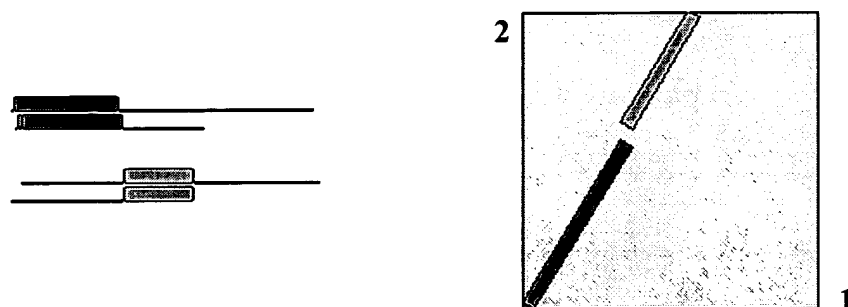
## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

SE8  
4/19/609

Sequence 1 lcl|seq\_1 Length 3283 (1 .. 3283)

Sequence 2 gi 4191609 Length 2010 (1 .. 2010)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2090 bits (1087), Expect = 0.0  
 Identities = 1098/1101 (99%), Gaps = 1/1101 (0%)  
 Strand = Plus / Plus



Query: 40 gggagccgcgggctctcggggaagagacggatgatgaacaagctttaca  
 |||||  
 Sbjct: 18 gggagccgcggcctca-ggggaagagacggatgatgaacaagctttaca  
 IGF-II mRNA-binding protein 2 1 M N K L Y

Query: 100 agccccgcggtcaccgcccagacctccggcagctctttggggacagga  
 |||||  
 Sbjct: 77 agccccgcggtcaccgcccagacctccggcagctctttggggacagga  
 IGF-II mRNA-binding protein 2 10 S P A V T A D D L R Q L F G D R

Query: 160 gcgggacaggtcctgctgaagtccggctacgccttcgtggactaccccg  
 |||||  
 Sbjct: 137 gcgggacaggtcctgctgaagtccggctacgccttcgtggactaccccg  
 IGF-II mRNA-binding protein 2 30 A G Q V L L K S G Y A F V D Y P

Query: 220 gccatccgcgccatcgagaccctctcgggtaaagtggaattgcatggga  
 |||||  
 Sbjct: 197 gccatccgcgccatcgagaccctctcgggtaaagtggaattgcatggga  
 IGF-II mRNA-binding protein 2 50 A I R A I E T L S G K V E L H G

```
Query:                280  gttgattactcagtcctctaaaaagctaaggagcaggaaaattcagattc
                        |||
Sbjct:                257  gttgattactcagtcctctaaaaagctaaggagcaggaaaattcagattc
IGF-II mRNA-binding protein 2 70  V D Y S V S K K L R S R K I Q I

Query:                340  cctcacctgcagtgagggtgttggtggacttttggctcaatatggga
                        |||
Sbjct:                317  cctcacctgcagtgagggtgttggtggacttttggctcaatatggga
IGF-II mRNA-binding protein 2 90  P H L Q W E V L D G L L A Q Y G

Query:                400  gtggaacaagtcaacacagacacagaaaccgccgttgtcaacgtcacat
                        |||
Sbjct:                377  gtggaacaagtcaacacagacacagaaaccgccgttgtcaacgtcacat
IGF-II mRNA-binding protein 2 110 V E Q V N T D T E T A V V N V T

Query:                460  gaagaagcaaaaatagccatggagaagctaagcgggcatcagtttgaga
                        |||
Sbjct:                437  gaagaagcaaaaatagccatggagaagctaagcgggcatcagtttgaga
IGF-II mRNA-binding protein 2 130 E E A K I A M E K L S G H Q F E

Query:                520  aagatttcctacatcccggatgaagaggtgagctccccttcgccccctc
                        |||
Sbjct:                497  aagatttcctacatcccggatgaagaggtgagctccccttcgccccctc
IGF-II mRNA-binding protein 2 150 K I S Y I P D E E V S S P S P P

Query:                580  cgtggggaccactcttcccgggagcaaggccacgcccctgggggcactt
                        |||
Sbjct:                557  cgtggggaccactcttcccgggagcaaggccacgcccctgggggcactt
IGF-II mRNA-binding protein 2 170 R G D H S S R E Q G H A P G G T

Query:                640  cagattgatttcccgtgcggatcctgggtccccaccagtttggttggtg
                        |||
Sbjct:                617  cagattgatttcccgtgcggatcctgggtccccaccagtttggttggtg
IGF-II mRNA-binding protein 2 190 Q I D F P L R I L V P T Q F V G

Query:                700  aaggagggccttgaccataaagaacatcactaagcagaccagtcgccggg
                        |||
Sbjct:                677  aaggagggccttgaccataaagaacatcactaagcagaccagtcgccggg
IGF-II mRNA-binding protein 2 210 K E G L T I K N I T K Q T Q S R

Query:                760  agaaaagagaactctggagctgcagagaagcctgtcaccatccatgccca
                        |||
Sbjct:                737  agaaaagagaactctggagctgcagagaagcctgtcaccatccatgccca
IGF-II mRNA-binding protein 2 230 R K E N S G A A E K P V T I H A

Query:                820  acttctgaagcatgccgcattgattccttgaaatcatgcagaaagaggcag
                        |||
Sbjct:                797  acttctgaagcatgccgcattgattccttgaaatcatgcagaaagaggcag
IGF-II mRNA-binding protein 2 250 T S E A C R M I L E I M Q K E A

Query:                880  ctagccgaagagattcctctgaaaatcctggcacacaatggcttggttg
                        |||
Sbjct:                857  ctagccgaagagattcctctgaaaatcctggcacacaatggcttggttg
```

IGF-II mRNA-binding protein 2 270 L A E E I P L K I L A H N G L V

Query: 940 ggaaaagaaggcagaaatttgaagaaaattgaacatgaaacagggacca  
Sbjct: 917 ggaaaagaaggcagaaatttgaagaaaattgaacatgaaacagggacca  
IGF-II mRNA-binding protein 2 290 G K E G R N L K K I E H E T G T

Query: 1000 tcatctttgcaggatttgagcatatacaaccggaagaaccatcactg  
Sbjct: 977 tcatctttgcaggatttgagcatatacaaccggaagaaccatcactg  
IGF-II mRNA-binding protein 2 310 S S L Q D L S I Y N P E R T I T

Query: 1060 gttgaggcctgtgccagtgtgagatagagattatgaagaagctgcgtg  
Sbjct: 1037 gttgaggcctgtgccagtgtgagatagagattatgaagaagctgcgtg  
IGF-II mRNA-binding protein 2 330 V E A C A S A E I E I M K K L R

Query: 1120 aatgatatgctggctgtaac 1140  
Sbjct: 1097 aatgatatgctggctgtaac 1117  
IGF-II mRNA-binding protein 2 350 N D M L A V N

Score = 1469 bits (764), Expect = 0.0  
Identities = 764/764 (100%)  
Strand = Plus / Plus

Query: 1141 acccactccggatacttctccagcctgtacccccatcaccagtttggcc  
Sbjct: 1247 acccactccggatacttctccagcctgtacccccatcaccagtttggcc  
IGF-II mRNA-binding protein 2 400 T H S G Y F S S L Y P H H Q F G

Query: 1201 catcactcttatccagagcaggagattgtgaatctcttcacccaaccc  
Sbjct: 1307 catcactcttatccagagcaggagattgtgaatctcttcacccaaccc  
IGF-II mRNA-binding protein 2 420 H H S Y P E Q E I V N L F I P T

Query: 1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg  
Sbjct: 1367 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg  
IGF-II mRNA-binding protein 2 440 A I I G K K G A H I K Q L A R F

Query: 1321 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatgggtca  
Sbjct: 1427 atcaagattgcccctgcggaaggcccagacgtcagcgaaaggatgggtca  
IGF-II mRNA-binding protein 2 460 I K I A P A E G P D V S E R M V

Query: 1381 ccaccggaagcccagttcaaggcccagggacggatctttgggaaactga  
Sbjct: 1487 ccaccggaagcccagttcaaggcccagggacggatctttgggaaactga  
IGF-II mRNA-binding protein 2 480 P P E A Q F K A Q G R I F G K L

Query: 1441 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc  
Sbjct: 1547 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc

```

Sbjct:                               1547 ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtg
IGF-II mRNA-binding protein 2 500   F F N P K E E V K L E A H I R V

Query:                               1501 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
                               |||
Sbjct:                               1607 gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
IGF-II mRNA-binding protein 2 520   A G R V I G K G G K T V N E L Q

Query:                               1561 gcagaagtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaag
                               |||
Sbjct:                               1667 gcagaagtcatcgtgcctcgtgaccaaaccgagatgaaaatgaggaag
IGF-II mRNA-binding protein 2 540   A E V I V P R D Q T P D E N E E

Query:                               1621 attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
                               |||
Sbjct:                               1727 attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
IGF-II mRNA-binding protein 2 560   I I G H F F A S Q T A Q R K I R

Query:                               1681 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
                               |||
Sbjct:                               1787 caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
IGF-II mRNA-binding protein 2 580   Q V K Q Q E Q K Y P Q G V A S Q

Query:                               1741 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
                               |||
Sbjct:                               1847 ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaac

Query:                               1801 tgagaccaaaccgagccagccagatcgggagcaaaccaaagaccatctg
                               |||
Sbjct:                               1907 tgagaccaaaccgagccagccagatcgggagcaaaccaaagaccatctg

Query:                               1861 gtctgcgaggcgccagggactctgccgaggccctgagaaccc 1904
                               |||
Sbjct:                               1967 gtctgcgaggcgccagggactctgccgaggccctgagaaccc 2010

CPU time:      0.04 user secs.      0.01 sys. secs      0.05 total secs.

Lambda      K      H
1.33      0.621      1.12

Gapped
Lambda      K      H
1.33      0.621      1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 9
Number of Sequences: 0
Number of extensions: 9
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 4
length of query: 3283
length of database: 8,918,056,233

```

effective HSP length: 26  
effective length of query: 3257  
effective length of database: 8,918,056,207  
effective search space: 29046109066199  
effective search space used: 29046109066199  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 22 (43.0 bits)

 **NCBI**  
Nucleotide Protein Translations Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (556 letters)

The request ID is 1061925537-609-1058353.BLASTQ3

p62 in  
pat  
database

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment  in HTML

Number of: Descriptions 100  Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by  or select from: (none)

Expect value range:



# results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1061916244-523-2727514.BLASTQ3

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,886,208 sequences; 8,918,056,233 total letters

Taxonomy reports

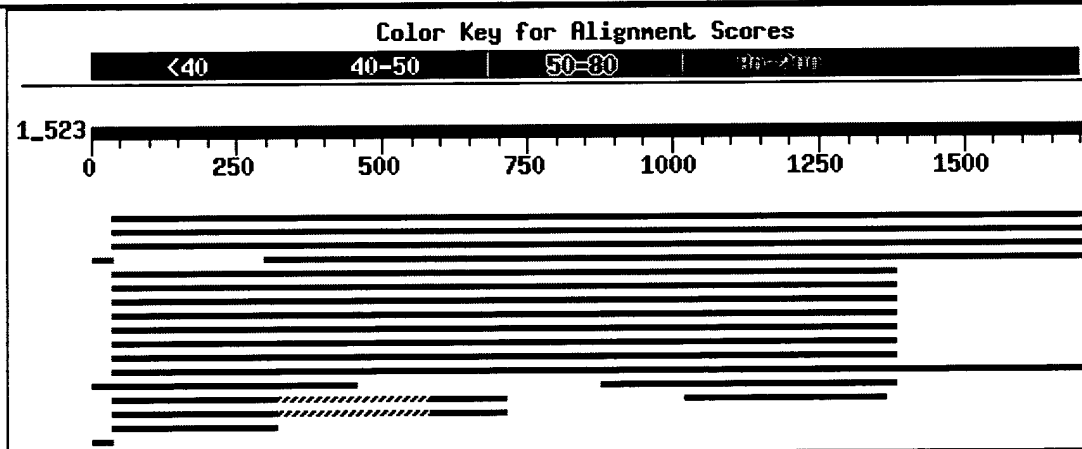
**Query=**

(1708 letters)

SEQ 5

## Distribution of 33 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:					Score (bits)	E Value
gi	4191607	gb	AF117106.1	AF117106 Homo sapiens IGF-II mRNA...	3167	0.0
gi	21361351	ref	NM 006546.2	Homo sapiens IGF-II mRNA-bindi...	3130	0.0
gi	7141071	gb	AF198254.1	AF198254 Homo sapiens mRNA-binding...	3130	0.0
gi	22760672	dbj	AK074915.1	Homo sapiens cDNA FLJ90434 fis,...	2663	0.0
gi	31342209	ref	NM 175594.2	Rattus norvegicus IGF-II mRNA...	1727	0.0
gi	27464837	gb	AF541940.1	Rattus norvegicus b-actin zipcod...	1727	0.0
gi	31560605	ref	NM 009951.2	Mus musculus insulin-like grow...	1675	0.0
gi	12851513	dbj	AK013940.1	Mus musculus 13 days embryo hea...	1675	0.0
gi	3273748	gb	AF061569.1	AF061569 Mus musculus coding regio...	1675	0.0
gi	26336870	dbj	AK044850.1	Mus musculus 9.5 days embryo pa...	1669	0.0
gi	30354043	gb	BC051679.1	Mus musculus insulin-like growth...	1669	0.0
gi	24580458	gb	AC105030.11	Homo sapiens chromosome 17, clo...	829	0.0
gi	21637524	gb	AC091133.11	Homo sapiens chromosome 17, clo...	546	e-152
gi	30581644	gb	AC094527.7	Rattus norvegicus 5 BAC CH230-4L...	477	e-131
gi	27689046	ref	XM 220886.1	Rattus norvegicus similar to I...	477	e-131
gi	22204252	emb	AL606704.20	Mouse DNA sequence from clone ...	344	2e-91
gi	21954991	gb	AC098642.5	Genomic sequence for Mus musculu...	344	2e-91
gi	14475918	gb	AC084407.10	Mus Musculus Strain C57BL6/J Ch...	344	2e-91

gi 15878883 emb AJ334465.1 HSA334465	Homo sapiens genomic s...	<u>70</u>	1e-08
gi 15876265 emb AJ331847.1 HSA331847	Homo sapiens genomic s...	<u>70</u>	1e-08

## Alignments

>gi|4191607|gb|AF117106.1|AF117106 Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1)  
Length = 2130

Score = 3167 bits (1647), Expect = 0.0  
Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)  
Strand = Plus / Plus

Query: 37	agccatcatgaagctgaatggccaccagttggagaaccatgcctgaaggtctcctacat	96
Sbjct: 411	agccatcatgaagctgaatggccaccagttggagaaccatgcctgaaggtctcctacat	470
Query: 97	ccccgatgagcagatagcacaggacctgagaatggcgccgaggggctttggctctcg	156
Sbjct: 471	ccccgatgagcagatagcacaggacctgagaatggcgccgaggggctttggctctcg	530
Query: 157	gggtcagccccgccagggtcacctgtggcagcggggccccagccaagcagcagcaagt	216
Sbjct: 531	gggtcagccccgccagggtcacctgtggcagcggggccccagccaagcagcagcaagt	590
Query: 217	ggacatcccccttcggctcctggtgcccaccagtatgtgggtgccattattggcaagga	276
Sbjct: 591	ggacatcccccttcggctcctggtgcccaccagtatgtgggtgccattattggcaagga	650
Query: 277	gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa	336
Sbjct: 651	gggggccaccatccgcaacatcacaaaacagaccagtcgaagatagacgtgcataggaa	710
Query: 337	ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccctgagggctgctc	396
Sbjct: 711	ggagaacgcaggtgcagctgaaaaagccatcagtgtgcactccaccctgagggctgctc	770
Query: 397	ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacaccaaaacggc	456
Sbjct: 771	ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggacaccaaaacggc	830
Query: 457	tgacgaggttcccctgaagatcctggcccataataactttgtagggcgtctcattggcaa	516
Sbjct: 831	tgacgaggttcccctgaagatcctggcccataataactttgtagggcgtctcattggcaa	890
Query: 517	ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc	576
Sbjct: 891	ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatcaccatctcctc	950
Query: 577	gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga	636
Sbjct: 951	gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaagggggccatcga	1010
Query: 637	gaattgttgaggccgagcaggaaataatgaagaaagtgcggaggcctatgagaatga	696



 **NCBI**  
Nucleotide      Protein      Translations      Retrieve results for an RID

formatting **BLAST**

Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

*megablast  
SEQ 5*

The request ID is

**Format!** or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi  in

Number of: Descriptions  Alignments

Alignment view

Start formatting  
from query #

Limit results by  or select from:

Expect value  
range:

Results file ☐



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

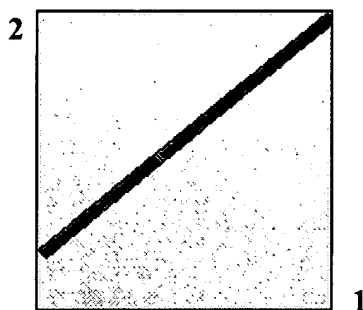
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lcl|seq\_1 Length 1708 (1 .. 1708)

Sequence 2 gi 4191607 Length 2130 (1 .. 2130)



seq 5  
4191607

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3163 bits (1645), Expect = 0.0  
 Identities = 1667/1678 (99%), Gaps = 6/1678 (0%)  
 Strand = Plus / Plus

Query: 37 agccatcatgaagctgaatggccaccagttggagaacctatgcctgaag  
 |||  
 Sbjct: 411 agccatcatgaagctgaatggccaccagttggagaacctatgcctgaag  
 IGF-II mRNA-binding protein 1 135 A I M K L N G H Q L E N H A L K

Query: 97 ccccgatgagcagatagcacagggacctgagaatggcgccgagggggc  
 |||  
 Sbjct: 471 ccccgatgagcagatagcacagggacctgagaatggcgccgagggggc  
 IGF-II mRNA-binding protein 1 155 P D E Q I A Q G P E N G R R G G

Query: 157 gggtcagccccgccagggctcacctgtggcagcgggggccccagccaag  
 |||  
 Sbjct: 531 gggtcagccccgccagggctcacctgtggcagcgggggccccagccaag  
 IGF-II mRNA-binding protein 1 175 G Q P R Q G S P V A A G A P A K

Query: 217 ggacatcccccttcggctcctggtgccaccagtatgtgggtgccatt  
 |||  
 Sbjct: 591 ggacatcccccttcggctcctggtgccaccagtatgtgggtgccatt  
 IGF-II mRNA-binding protein 1 195 D I P L R L L V P T Q Y V G A I

```
Query:          277  gggggccaccatccgcaacatcacaaaacagaccaggtccaagatagac
                   |||
Sbjct:          651  gggggccaccatccgcaacatcacaaaacagaccaggtccaagatagac
IGF-II mRNA-binding protein 1 215  G A T I R N I T K Q T Q S K I D

Query:          337  ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccct
                   |||
Sbjct:          711  ggagaacgcaggtgcagctgaaaaagccatcagtggtgcactccaccct
IGF-II mRNA-binding protein 1 235  E N A G A A E K A I S V H S T P

Query:          397  ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggac
                   |||
Sbjct:          771  ctccgcttgtaagatgatcttgagattatgcataaagaggctaaggac
IGF-II mRNA-binding protein 1 255  S A C K M I L E I M H K E A K D

Query:          457  tgacgaggttccccctgaagatcctggcccataataactttgtagggcgt
                   |||
Sbjct:          831  tgacgaggttccccctgaagatcctggcccataataactttgtagggcgt
IGF-II mRNA-binding protein 1 275  D E V P L K I L A H N N F V G R

Query:          517  ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatc
                   |||
Sbjct:          891  ggaaggacggaacctgaagaaggtagagcaagataccgagacaaaaatc
IGF-II mRNA-binding protein 1 295  E G R N L K K V E Q D T E T K I

Query:          577  gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaag
                   |||
Sbjct:          951  gttgcaagaccttaccctttacaaccctgagaggaccatcactgtgaag
IGF-II mRNA-binding protein 1 315  L Q D L T L Y N P E R T I T V K

Query:          637  gaattgttgcaaggccgagcaggaaataatgaagaaagttcgggaggcc
                   |||
Sbjct:          1011  gaattgttgcaaggccgagcaggaaataatgaagaaagttcgggaggcc
IGF-II mRNA-binding protein 1 335  N C C R A E Q E I M K K V R E A

Query:          697  tgtggctgcatgagc-----tctcacctgatccctggcctgaacctg
                   |||
Sbjct:          1071  tgtggctgcatgagcctgcagtctcacctgatccctggcctgaacctg
IGF-II mRNA-binding protein 1 355  V A A M S L Q S H L I P G L N L

Query:          751  tcttttccagcttcatccagcgcagtcctcgccgctccagcagcggtt
                   |||
Sbjct:          1131  tcttttccagcttcatccagcgcagtcctcgccgctccagcagcggtt
IGF-II mRNA-binding protein 1 375  L F P A S S S A V P P P P S S V

Query:          811  tccctatagctcctttatgcaggctcccagcaggagatggtgcaggtg
                   |||
Sbjct:          1191  tccctatagctcctttatgcaggctcccagcaggagatggtgcaggtg
IGF-II mRNA-binding protein 1 395  P Y S S F M Q A P E Q E M V Q V

Query:          871  ccaggcagtgggcgccatcatcggcaagaaggggcagcacatcaaacag
                   |||
Sbjct:          1251  ccaggcagtgggcgccatcatcggcaagaaggggcagcacatcaaacag
```

```
Query:      1531 ctntcagccccaacacccacccaattggcccaacactgtntgccctc
             |||||||||||||||||||||||||||||||||||
Sbjct:      1911 ctctcagccccaacacccacccaattggcccaacactgtctgccctc
```

Query: 1591 aatntagcgcaaggcacttttaaacgtggattgtttaagaagctctc  
||| |  
Sbjct: 1971 aattctagcgcaaggcacttttaaacgtggattgtttaagaagctctc

Query: 1651 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcag  
||| |  
Sbjct: 2031 aagaggggtggatcacacctcagtgggaagaaaaataaaatttccttcag

CPU time: 0.00 user secs. 0.02 sys. secs 0.02 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 12  
Number of Sequences: 0  
Number of extensions: 12  
Number of successful extensions: 2  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 1708  
length of database: 8,918,056,233  
effective HSP length: 25  
effective length of query: 1683  
effective length of database: 8,918,056,208  
effective search space: 15009088598064  
effective search space used: 15009088598064  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

●MIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

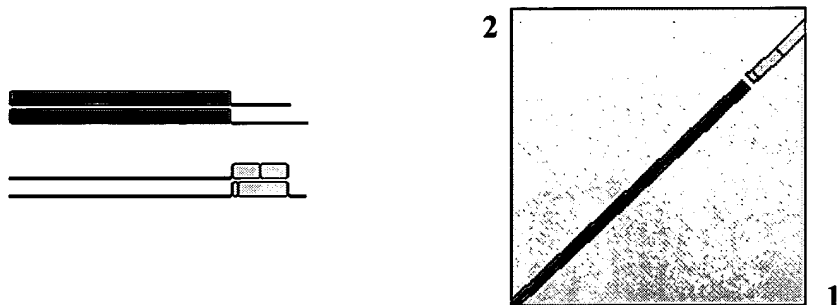
Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lcl|seq\_1

Length 3412 (1 .. 3412)

Sequence 2 gi 27552765 Homo sapiens IGF-II mRNA-binding protein 2  
 (IMP-2), mRNA

Length 3642 (1 .. 3642)



SEQ 6  
 gi 27552765

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 5107 bits (2656), Expect = 0.0  
 Identities = 2671/2686 (99%)  
 Strand = Plus / Plus



```

Query:          5      gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggct
                   |||
Sbjct:          9      gcggaggaggcgaggagcgccgggtaccgggcccggggagccgcgggct

Query:        65      gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcac
                   |||
Sbjct:        69      gacggatgatgaacaagctttacatcgggaaacctgagccccgccgtcac
IGF-II mRNA-binding protein 2 1      M N K L Y I G N L S P A V T

Query:        125     tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
                   |||
Sbjct:        129     tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
IGF-II mRNA-binding protein 2 18     L R Q L F G D R K L P L A G Q V L

Query:        185     gctacgccttcgtggactacccgaccagaactgggcatccgcgcat
                   |||
Sbjct:        189     gctacgccttcgtggactacccgaccagaactgggcatccgcgcat
  
```

IGF-II mRNA-binding protein 2	38	G	Y	A	F	V	D	Y	P	D	Q	N	W	A	I	R	A	I
Query:	245	cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt																
Sbjct:	249	cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt																
IGF-II mRNA-binding protein 2	58	S	G	K	V	E	L	H	G	K	I	M	E	V	D	Y	S	V
Query:	305	taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtg																
Sbjct:	309	taaggagcaggaaaattcagattcgaaacatccctcctcacctgcagtg																
IGF-II mRNA-binding protein 2	78	L	R	S	R	K	I	Q	I	R	N	I	P	P	H	L	Q	W
Query:	365	atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa																
Sbjct:	369	atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa																
IGF-II mRNA-binding protein 2	98	D	G	L	L	A	Q	Y	G	T	V	E	N	V	E	Q	V	N
Query:	425	aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaat																
Sbjct:	429	aaaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaaat																
IGF-II mRNA-binding protein 2	118	E	T	A	V	V	N	V	T	Y	A	T	R	E	E	A	K	I
Query:	485	agctaagcgggcatcagtttgagaactactccttcaagatttcctacat																
Sbjct:	489	agctaagcgggcatcagtttgagaactactccttcaagatttcctacat																
IGF-II mRNA-binding protein 2	138	K	L	S	G	H	Q	F	E	N	Y	S	F	K	I	S	Y	I
Query:	545	aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactc																
Sbjct:	549	aggtgagctccccttcgccccctcagcgagcccagcgtggggaccactc																
IGF-II mRNA-binding protein 2	158	E	V	S	S	P	S	P	P	Q	R	A	Q	R	G	D	H	S
Query:	605	aaggccacgcccctgggggcacttctcaggccagacagattgatttccc																
Sbjct:	609	aaggccacgcccctgggggcacttctcaggccagacagattgatttccc																
IGF-II mRNA-binding protein 2	178	Q	G	H	A	P	G	G	T	S	Q	A	R	Q	I	D	F	P
Query:	665	tggtccccaccagtttggttggtgccatcatcggaaggagggttgac																
Sbjct:	669	tggtccccaccagtttggttggtgccatcatcggaaggagggttgac																
IGF-II mRNA-binding protein 2	198	L	V	P	T	Q	F	V	G	A	I	I	G	K	E	G	L	T
Query:	725	tactaagcagaccagtcgccgggtagatatccatagaaaagagaactc																
Sbjct:	729	tactaagcagaccagtcgccgggtagatatccatagaaaagagaactc																
IGF-II mRNA-binding protein 2	218	I	T	K	Q	T	Q	S	R	V	D	I	H	R	K	E	N	S
Query:	785	agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatg																
Sbjct:	789	agaagcctgtcaccatccatgccaccccagaggggacttctgaagcatg																
IGF-II mRNA-binding protein 2	238	E	K	P	V	T	I	H	A	T	P	E	G	T	S	E	A	C
Query:	845	ttgaaatcatgcagaaagaggcagatgagaccaaactagccgaagagat																

Sbjct:	849	ttgaaatcatgcagaaagaggcagatgagaccaaaactagccgaagagat
IGF-II mRNA-binding protein 2	258	L E I M Q K E A D E T K L A E E I
Query:	905	tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcag
Sbjct:	909	tcttggcacacaatggcttgggttgaagactgattggaaaagaaggcag
IGF-II mRNA-binding protein 2	278	I L A H N G L V G R L I G K E G R
Query:	965	aaattgaacatgaaacagggaccaagataacaatctcatctttgcagga
Sbjct:	969	aaattgaacatgaaacagggaccaagataacaatctcatctttgcagga
IGF-II mRNA-binding protein 2	298	K I E H E T G T K I T I S S L Q D
Query:	1025	acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgc
Sbjct:	1029	acaaccggaagaaccatcactgtgaagggcacagttgaggcctgtgc
IGF-II mRNA-binding protein 2	318	Y N P E R T I T V K G T V E A C A
Query:	1085	tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc
Sbjct:	1089	tagagattatgaagaagctgcgtgaggcctttgaaaatgatatgctggc
IGF-II mRNA-binding protein 2	338	I E I M K K L R E A F E N D M L A
Query:	1145	aagccaatctgatcccaggggtgaacctcagcgcacttggcatcttttc
Sbjct:	1149	aagccaatctgatcccaggggtgaacctcagcgcacttggcatcttttc
IGF-II mRNA-binding protein 2	358	Q A N L I P G L N L S A L G I F S
Query:	1205	ccgtgctatctccaccagcagggcccccgcggagctcccccgctgcccc
Sbjct:	1209	ccgtgctatctccaccagcagggcccccgcggagctcccccgctgcccc
IGF-II mRNA-binding protein 2	378	S V L S P P A G P R G A P P A A P
Query:	1265	tcaactaccactccggatacttctccagcctgtacccccatcaccagtt
Sbjct:	1269	tcaactaccactccggatacttctccagcctgtacccccatcaccagtt
IGF-II mRNA-binding protein 2	398	F T T H S G Y F S S L Y P H H Q F
Query:	1325	cgcacatcactcttatccagagcaggagattgtgaatctcttcatccc
Sbjct:	1329	cgcacatcactcttatccagagcaggagattgtgaatctcttcatccc
IGF-II mRNA-binding protein 2	418	P H H H S Y P E Q E I V N L F I P
Query:	1385	tgggcgccatcatcggaagaagggggcacacatcaaacagctggcgag
Sbjct:	1389	tgggcgccatcatcggaagaagggggcacacatcaaacagctggcgag
IGF-II mRNA-binding protein 2	438	V G A I I G K K G A H I K Q L A R
Query:	1445	cctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggat
Sbjct:	1449	cctctatcaagattgccctgcggaaggcccagacgtcagcgaaaggat
IGF-II mRNA-binding protein 2	458	A S I K I A P A E G P D V S E R M
Query:	1505	ccggggccaccggaagcccagttcaaggcccaggacggatctttgggaa



```

Sbjct: 1509 cccgggccaccggaagcccagttcaaggcccaggacggatctttgggaa
IGF-II mRNA-binding protein 2 478 T G P P E A Q F K A Q G R I F G K

Query: 1565 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcag
Sbjct: 1569 aaaacttctttaaccccaaagaagaagtgaagctggaagcgcatatcag
IGF-II mRNA-binding protein 2 498 E N F F N P K E E V K L E A H I R

Query: 1625 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaact
Sbjct: 1629 ccacagctggccgggtgattggcaaaggtggcaagaccgtgaacgaact
IGF-II mRNA-binding protein 2 518 S T A G R V I G K G G K T V N E L

Query: 1685 ccagtgcagaagtcatcgtgcctcgtgaccaaacgccagatgaaaatga
Sbjct: 1689 ccagtgcagaagtcatcgtgcctcgtgaccaaacgccagatgaaaatga
IGF-II mRNA-binding protein 2 538 T S A E V I V P R D Q T P D E N E

Query: 1745 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagat
Sbjct: 1749 tcagaattatcgggcacttctttgctagccagactgcacagcgcaagat
IGF-II mRNA-binding protein 2 558 V R I I G H F F A S Q T A Q R K I

Query: 1805 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctc
Sbjct: 1809 tacaacaggtgaagcagcaggagcagaaataccctcagggagtcgcctc
IGF-II mRNA-binding protein 2 578 V Q Q V K Q Q E Q K Y P Q G V A S

Query: 1865 agtgaggctccacaggcaccagcaaaacaacggatgaatgtagccctt
Sbjct: 1869 agtgaggctccacaggcaccagcaaaacaacggatgaatgtagccctt
IGF-II mRNA-binding protein 2 598 K ^^^

Query: 1925 cagaatgagaccaaacgcagccagccagatcgggagcaaaccaagacc
Sbjct: 1929 cagaatgagaccaaacgcagccagccagatcgggagcaaaccaagacc

Query: 1985 gagaagtctgcggaggcggccagggactctgccgaggccctgagaacct
Sbjct: 1989 gagaagtctgcggaggcggccagggactctgccgaggccctgagaacct

Query: 2045 gaggggcggggaaggtcagccaggtttgccagaaccaccgagccccgcc
Sbjct: 2049 gaggggcggggaaggtcagccaggtttgccagaaccaccgagccccgcc

Query: 2105 agggcttctgcaggcttcagccatccacttcaccatccactcggatctc
Sbjct: 2109 agggcttctgcaggcttcagccatccacttcaccatccactcggatctc

Query: 2165 cacgacgctatcccttttagttgaactaacataggtgaacgtgttcaaa
Sbjct: 2169 cacgacgctatcccttttagttgaactaacataggtgaacgtgttcaaa
```

Query: 2225 tgcacaccctttttctgtggcaaatacgtctctgtacatgtgtgtacata  
|||||  
Sbjct: 2229 tgcacaccctttttctgtggcaaatacgtctctgtacatgtgtgtacata

Query: 2285 agatgttaagatatgtggcctgtgggttacacaggggtgcctgcagcgg  
|||||  
Sbjct: 2289 agatgttaagatatgtggcctgtgggttacacaggggtgcctgcagcgg

Query: 2345 gaaataatatatcaaataactcaactaactccaatttttaataatcaattat  
|||||  
Sbjct: 2349 gaaataatatatcaaataactcaactaactccaatttttaataatcaattat

Query: 2405 nnnnnnnaagagaaagcaggcttttctagactttaagaataaagtct  
|||||  
Sbjct: 2409 tctttttaagagaaagcaggcttttctagactttaagaataaagtct

Query: 2465 cacgggtgtagagaggagctttgaggccacccgcacaaaattcacccaga  
|||||  
Sbjct: 2469 cacgggtgtagagaggagctttgaggccacccgcacaaaattcacccaga

Query: 2525 tcggaaggacactcacggcagttctggatcacctgtgtatgtcaacaga  
|||||  
Sbjct: 2529 tcggaaggacactcacggcagttctggatcacctgtgtatgtcaacaga

Query: 2585 ctccttgaagaggaaactctgtcactcctcatgcctgtctagctcatac  
|||||  
Sbjct: 2589 ctccttgaagaggaaactctgtcactcctcatgcctgtctagctcatac

Query: 2645 tttgcttcacagggttttaactgggtttttgcatactgctatataa 26  
|||||  
Sbjct: 2649 tttgcttcacagggttttaactgggtttttgcatactgctatataa 26

Score = 1040 bits (541), Expect = 0.0  
Identities = 609/665 (91%), Gaps = 2/665 (0%)  
Strand = Plus / Plus



Query: 2749 cattcttttgaatttcctcatccctccatctcaatcccgatctacgcannnnnnnnnnn 2808  
|||||  
Sbjct: 2753 cattcttttgaatttcctcatccctccatctcaatcccgatctacgcacccccccccc 2812

Query: 2809 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2868  
|||||  
Sbjct: 2813 c-aggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2871

Query: 2869 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgccta 2928  
|||||  
Sbjct: 2872 aaccagcctcaacttacacttggttactcaaaagaacaagagtcaatggtacttgccta 2931

Query: 2929 gcgttttgggaagaggaaaacaggaacccaccaaaccaatcaaccaaacaagaaaa 2988  
|||||  
Sbjct: 2932 gcgttttgggaagaggaaaacaggaacccaccaaaccaatcaaccaaacaagaaaa 2991

```

Query: 2989 aattccacaatgaaagaatgtatcttcttttgcattttggtgtataagccatcaata 3048
          |||
Sbjct: 2992 aattccacaatgaaagaatgtatcttcttttgcattttggtgtataagccatcaata 3051

Query: 3049 ttcagcaaatgattcctttcttt-nnnnnnnnnnnntgtggaggaaagtagaaatttacc 3107
          |||
Sbjct: 3052 ttcagcaaatgattcctttcttttaaaaaaaaaaaaatgtggaggaaagtagaaatttacc 3111

Query: 3108 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3167
          |||
Sbjct: 3112 aaggttggtggcccgaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3171

Query: 3168 gaagctacctcaggtgtttttacctcagcaccttgctcttggtgtttcccttagagatttt 3227
          |||
Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgctcttggtgtttcccttagagatttt 3231

Query: 3228 gtaaagctgatagttggagcannnnnnnnnnnnnnnaataaaaaatgagttggnnnnnnnnn 3287
          |||
Sbjct: 3232 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3291

Query: 3288 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3347
          |||
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3348 attgtcttccgctagccaagaacnataatggccttcttttgacaaaaccttgaaaatggt 3407
          |||
Sbjct: 3352 attgtcttccgctagccaagaacctataatggccttcttttgacaaaaccttgaaaatggt 3411

Query: 3408 tattt 3412
          |||
Sbjct: 3412 tattt 3416

```

CPU time: 0.06 user secs. 0.01 sys. secs 0.07 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 13  
 Number of Sequences: 0  
 Number of extensions: 13  
 Number of successful extensions: 8  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 2  
 length of query: 3412  
 length of database: 8,918,056,233  
 effective HSP length: 26

effective length of query: 3386  
effective length of database: 8,918,056,207  
effective search space: 30196538316902  
effective search space used: 30196538316902  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 22 (43.0 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

●MIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

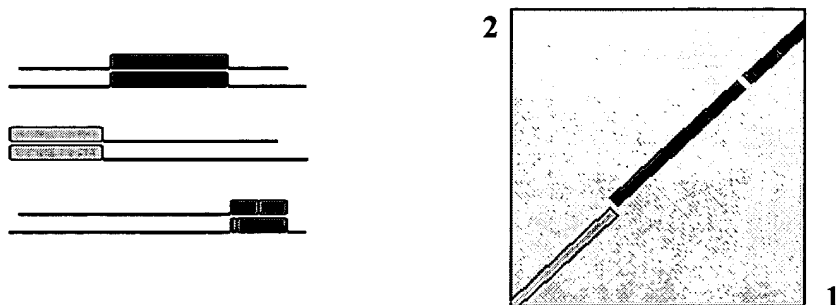
SE 8  
27552765

Sequence 1 lcl|seq\_1

Length 3283 (1 .. 3283)

Sequence 2 gi 27552765 Homo sapiens IGF-II mRNA-binding protein 2  
(IMP-2), mRNA

Length 3642 (1 .. 3642)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2675 bits (1391), Expect = 0.0  
 Identities = 1406/1421 (98%)  
 Strand = Plus / Plus

```

Query:                1141 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
                        |||
Sbjct:                1274 acccactccggatacttctccagcctgtacccccatcaccagtttggcc
IGF-II mRNA-binding protein 2 400  T H S G Y F S S L Y P H H Q F G
  
```

```

Query:                1201 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccc
                        |||
Sbjct:                1334 catcactcttatccagagcaggagattgtgaatctcttcatcccaaccc
IGF-II mRNA-binding protein 2 420  H H S Y P E Q E I V N L F I P T
  
```

```

Query:                1261 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
                        |||
Sbjct:                1394 gccatcatcggaagaagggggcacacatcaaacagctggcgagattcg
IGF-II mRNA-binding protein 2 440  A I I G K K G A H I K Q L A R F
  
```

```

Query:                1321 atcaagattgccctgcggaaggcccagacgtcagcgaaaggatgggtca
                        |||
  
```

Sbjct:	1454	atcaagattgccctgcggaaggcccgacgtcagcgaaaggatgggtca
IGF-II mRNA-binding protein 2	460	I K I A P A E G P D V S E R M V
Query:	1381	ccaccggaagcccagttcaaggcccaggacggatctttgggaaactga
Sbjct:	1514	ccaccggaagcccagttcaaggcccaggacggatctttgggaaactga
IGF-II mRNA-binding protein 2	480	P P E A Q F K A Q G R I F G K L
Query:	1441	ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc
Sbjct:	1574	ttctttaaccccaaagaagaagtgaagctggaagcgcatatcagagtgc
IGF-II mRNA-binding protein 2	500	F F N P K E E V K L E A H I R V
Query:	1501	gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
Sbjct:	1634	gctggccgggtgattggcaaaggtggcaagaccgtgaacgaactgcaga
IGF-II mRNA-binding protein 2	520	A G R V I G K G G K T V N E L Q
Query:	1561	gcagaagtcatcgtgcctcgtgaccaaaccgacagatgaaaatgaggaag
Sbjct:	1694	gcagaagtcatcgtgcctcgtgaccaaaccgacagatgaaaatgaggaag
IGF-II mRNA-binding protein 2	540	A E V I V P R D Q T P D E N E E
Query:	1621	attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
Sbjct:	1754	attatcgggcacttctttgctagccagactgcacagcgcaagatcaggg
IGF-II mRNA-binding protein 2	560	I I G H F F A S Q T A Q R K I R
Query:	1681	caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
Sbjct:	1814	caggtgaagcagcaggagcagaaataccctcagggagtcgcctcacagc
IGF-II mRNA-binding protein 2	580	Q V K Q Q E Q K Y P Q G V A S Q
Query:	1741	ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
Sbjct:	1874	ggctccacaggcaccagcaaaacaacggatgaatgtagcccttccaac
Query:	1801	tgagaccaaaccgagccagccagatcgggagcaaaacaaagaccatctg
Sbjct:	1934	tgagaccaaaccgagccagccagatcgggagcaaaacaaagaccatctg
Query:	1861	gtctgcggaggcggccagggaactctgccgaggccctgagaacccaggg
Sbjct:	1994	gtctgcggaggcggccagggaactctgccgaggccctgagaacccaggg
Query:	1921	gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccg
Sbjct:	2054	gcggggaaggtcagccaggtttgccagaaccaccgagccccgcctcccg
Query:	1981	ttctgcaggcttcagccatccacttcacatccactcggatctctcctg
Sbjct:	2114	ttctgcaggcttcagccatccacttcacatccactcggatctctcctg

```
Query:          2041 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaa
                  |||
Sbjct:          2174 cgctatcccttttagttgaactaacataggtgaacgtgttcaaagccaa

Query:          2101 accctttttctgtggcaaatacgctctctgtacatgtgtgtacatattaga
                  |||
Sbjct:          2234 accctttttctgtggcaaatacgctctctgtacatgtgtgtacatattaga

Query:          2161 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatat
                  |||
Sbjct:          2294 ttaagatatgtggcctgtgggttacacaggggtgcctgcagcggtaatat

Query:          2221 aatatatcaaataactcaactaactccaatttttaataattattaann
                  |||
Sbjct:          2354 aatatatcaaataactcaactaactccaatttttaataattattaatt

Query:          2281 nnaaagagaaagcaggcttttctagactttaagaataaagtctttggg
                  |||
Sbjct:          2414 ttaaagagaaagcaggcttttctagactttaagaataaagtctttggg

Query:          2341 tgtagagaggagctttgaggccaccgcacaaaattcaccagagggaa
                  |||
Sbjct:          2474 tgtagagaggagctttgaggccaccgcacaaaattcaccagagggaa

Query:          2401 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagga
                  |||
Sbjct:          2534 aggacactcacggcagttctggatcacctgtgtatgtcaacagaagga

Query:          2461 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccca
                  |||
Sbjct:          2594 tgaagaggaaactctgtcactcctcatgcctgtctagctcatacaccca

Query:          2521 ttcacaggttttaaaactgggtttttgcatactgctatataa 2561
                  |||
Sbjct:          2654 ttcacaggttttaaaactgggtttttgcatactgctatataa 2694
```

Score = 2184 bits (1136), Expect = 0.0

Identities = 1136/1136 (100%)

Strand = Plus / Plus



```
Query:          5   gcggaggaggcgaggagcgccgggtaccgggcccgggggagccgcgggct
                  |||
Sbjct:          9   gcggaggaggcgaggagcgccgggtaccgggcccgggggagccgcgggct

Query:          65   gacggatgatgaacaagctttacatcgggaacctgagccccgccgtcac
                  |||
Sbjct:          69   gacggatgatgaacaagctttacatcgggaacctgagccccgccgtcac
IGF-II mRNA-binding protein 2 1      M N K L Y I G N L S P A V T

Query:          125  tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
                  |||
Sbjct:          129  tccggcagctctttggggacaggaagctgccctggcgggacaggtcct
```

IGF-II mRNA-binding protein 2 18 L R Q L F G D R K L P L A G Q V L

```

Query:                185  gctacgccttcgtggactaccccgaccagaactgggccatccgcgccat
                        |||
Sbjct:                189  gctacgccttcgtggactaccccgaccagaactgggccatccgcgccat
IGF-II mRNA-binding  38  G Y A F V D Y P D Q N W A I R A I

```

```

Query:                245  cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt
                        |||
Sbjct:                249  cgggtaaagtggaattgcatgggaaaatcatggaagttgattactcagt
IGF-II mRNA-binding  58  S G K V E L H G K I M E V D Y S V

```

```

Query:                305  taaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtg
                        |||
Sbjct:                309  taaggagcagggaaaattcagattcgaaacatccctcctcacctgcagtg
IGF-II mRNA-binding protein 2 78  L R S R K I Q I R N I P P H L Q W

```

```

Query:                               365  atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa
                                   |||
Sbjct:                               369  atggacttttggctcaatatgggacagtggagaatgtggaacaagtcaa
IGF-II mRNA-binding protein 2 98  D G L L A Q Y G T V E N V E Q V N

```

```

Query:                425 aaaccgccggttgtaacgtcacatatgcaacaagagaagaagcaaaaat
                        |||
Sbjct:                429 aaaccgccggttgtaacgtcacatatgcaacaagagaagaagcaaaaat
IGF-II mRNA-binding 118 E T A V V N V T Y A T R E E A K I

```

```

Query:                485  agctaagcgggcatcagtttgagaactactccttcaagatttcctacat
                        |||
Sbjct:                489  agctaagcgggcatcagtttgagaactactccttcaagatttcctacat
IGF-II mRNA-binding protein 2 138  K L S G H Q F E N Y S F K I S Y I

```

```

Query:                545  aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc
                        |||
Sbjct:                549  aggtgagctcccttcgccccctcagcgagcccagcgtggggaccactc
IGF-II mRNA-binding  158  E V S S P S P P Q R A Q R G D H S

```

```

Query:                605  aagggcacgcccctgggggcacttctcaggccagacagattgatttccc
                        |||
Sbjct:                609  aagggcacgcccctgggggcacttctcaggccagacagattgatttccc
IGF-II mRNA-binding  178  Q G H A P G G T S Q A R Q I D F P

```

```

Query:                665  tgggtccccacccagtttggttggtgccatcatcggaaggagggttgac
                        |||
Sbjct:                669  tgggtccccacccagtttggttggtgccatcatcggaaggagggttgac
IGF-II mRNA-binding  198  L V P T Q F V G A I I G K E G L T

```

```

Query:              725  tcactaagcagacccagtcctcggttagatatccatagaaaagagaactc
                        |||
Sbjct:              729  tcactaagcagacccagtcctcggttagatatccatagaaaagagaactc
IGF-II mRNA-binding protein 2 218  I T K Q T Q S R V D I H R K E N S

```

Query: 785 agaagcctgtcaccatccatgccacccagaggggacttctgaagcatg



Query: 2860 aattccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaata 2919  
 |||  
 Sbjct: 2992 aattccacaatgaaagaatgtattttgtctttttgcattttgggtgtataagccatcaata 3051

Query: 2920 ttcagcaaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978  
|||||  
Sbjct: 3052 ttcagcaaaatgattcctttctttaaaaaaaaaaagtgaggaaagtagaaatttacc 3111

Query: 2979 aaggttggtggcccgaggcggttaaattcacagannnnnnnaacgagaaaaacacacagaa 3038  
|||||  
Sbjct: 3112 aaggttggtggcccgaggcggttaaattcacagatttttttaacgagaaaaacacacagaa 3171

Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3098  
|||||  
Sbjct: 3172 gaagctacctcaggtgtttttacctcagcaccttgctcttggtttcccttagagatttt 3231

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158  
|||||  
Sbjct: 3232 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3291

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218  
|||||  
Sbjct: 3292 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3351

Query: 3219 attgtcttccgctagccaagaacnataatggccttcttttgacaaaccttgaaaatgtt 3278  
|||||  
Sbjct: 3352 attgtcttccgctagccaagaacctataatggccttcttttgacaaaccttgaaaatgtt 3411

Query: 3279 tatttt 3283  
|||||  
Sbjct: 3412 tatttt 3416

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 14  
Number of Sequences: 0  
Number of extensions: 14  
Number of successful extensions: 9  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 5  
length of query: 3283  
length of database: 8,918,056,233  
effective HSP length: 26  
effective length of query: 3257  
effective length of database: 8,918,056,207  
effective search space: 29046109066199  
effective search space used: 29046109066199  
T: 0  
A: 0  
X1: 6 (11.5 bits)

X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 22 (43.0 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

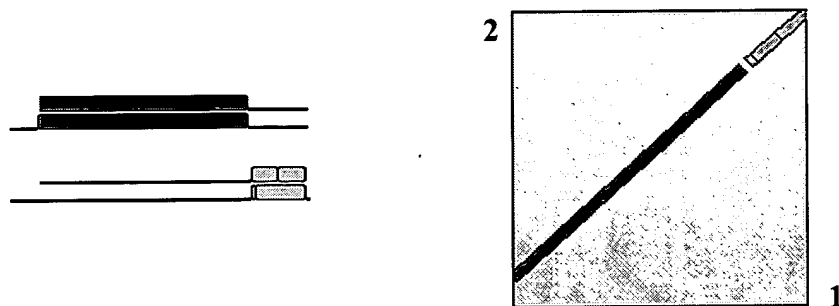
Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

SEQ 8  
gi 4883680

Sequence 1 lcl|seq\_1 Length 3283 (1 .. 3283)

Sequence 2 gi 4883680 Length 3667 (1 .. 3667)

(hepatocellular)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 4857 bits (2526), Expect = 0.0  
 Identities = 2541/2556 (99%)  
 Strand = Plus / Plus



```

Query:          6  cggaggaggcgaggagcgccgggtaccgggcccggggagccgcggg
                  |||
Sbjct:        372  cggaggaggcgaggagcgccgggtaccgggcccggggagccgcggg

Query:          66  acggatgatgaacaagctttacatcgggaaacctgagccccgccgtc
                  |||
Sbjct:        432  acggatgatgaacaagctttacatcgggaaacctgagccccgccgtc
hepatocellular carcinoma autoan> 1      M M N K L Y I G N L S P A V

Query:          126  ccggcagctctttggggacaggaagctgccctggcgggacaggtc
                  |||
Sbjct:        492  ccggcagctctttggggacaggaagctgccctggcgggacaggtc
hepatocellular carcinoma autoan> 20      R Q L F G D R K L P L A G Q V

Query:          186  ctacgccttcgtggactaccccgaccagaactgggcatccgcgcc
                  |||
Sbjct:        552  ctacgccttcgtggactaccccgaccagaactgggcatccgcgcc
hepatocellular carcinoma autoan> 40      Y A F V D Y P D Q N W A I R A
  
```

```
Query:          246  gggtaaagtggaattgcatgggaaaatcatggaagttgattactca
                   |||
Sbjct:          612  gggtaaagtggaattgcatgggaaaatcatggaagttgattactca
hepatocellular carcinoma autoan> 60      G K V E L H G K I M E V D Y S

Query:          306  aaggagcaggaaaattcagattcgaaacatccctcctcacctgcag
                   |||
Sbjct:          672  aaggagcaggaaaattcagattcgaaacatccctcctcacctgcag
hepatocellular carcinoma autoan> 80      R S R K I Q I R N I P P H L Q

Query:          366  tggacttttggctcaatatgggacagtggagaatgtggaacaagtc
                   |||
Sbjct:          732  tggacttttggctcaatatgggacagtggagaatgtggaacaagtc
hepatocellular carcinoma autoan> 100     G L L A Q Y G T V E N V E Q V

Query:          426  aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaa
                   |||
Sbjct:          792  aaccgccgttgtcaacgtcacatatgcaacaagagaagaagcaaaa
hepatocellular carcinoma autoan> 120     T A V V N V T Y A T R E E A K

Query:          486  gctaagcgggcatcagtttgagaactactccttcaagatttcctac
                   |||
Sbjct:          852  gctaagcgggcatcagtttgagaactactccttcaagatttcctac
hepatocellular carcinoma autoan> 140     L S G H Q F E N Y S F K I S Y

Query:          546  ggtgagctccccttcgccccctcagcgagcccagcgtggggaccac
                   |||
Sbjct:          912  ggtgagctccccttcgccccctcagcgagcccagcgtggggaccac
hepatocellular carcinoma autoan> 160     V S S P S P P Q R A Q R G D H

Query:          606  aggccacgcccctgggggcacttctcaggccagacagattgatttc
                   |||
Sbjct:          972  aggccacgcccctgggggcacttctcaggccagacagattgatttc
hepatocellular carcinoma autoan> 180     G H A P G G T S Q A R Q I D F

Query:          666  ggtccccacccagtttggttggtgccatcatcggaaggagggttg
                   |||
Sbjct:          1032 ggtccccacccagtttggttggtgccatcatcggaaggagggttg
hepatocellular carcinoma autoan> 200     V P T Q F V G A I I G K E G L

Query:          726  cactaagcagaccagtcgccgggtagatatccatagaaaagagaaac
                   |||
Sbjct:          1092 cactaagcagaccagtcgccgggtagatatccatagaaaagagaaac
hepatocellular carcinoma autoan> 220     T K Q T Q S R V D I H R K E N

Query:          786  gaagcctgtcaccatccatgccaccccagaggggacttctgaagca
                   |||
Sbjct:          1152 gaagcctgtcaccatccatgccaccccagaggggacttctgaagca
hepatocellular carcinoma autoan> 240     K P V T I H A T P E G T S E A

Query:          846  tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagag
                   |||
Sbjct:          1212 tgaaatcatgcagaaagaggcagatgagaccaaactagccgaagag
hepatocellular carcinoma autoan> 260     E I M Q K E A D E T K L A E E
```

```
Query:          906 cttggcacacaatggcttggttgggaagactgattggaaaagaaggc
                  |||
Sbjct:          1272 cttggcacacaatggcttggttgggaagactgattggaaaagaaggc
hepatocellular carcinoma autoan> 280 L A H N G L V G R L I G K E G

Query:          966 aattgaacatgaaacagggaccaagataacaatctcatctttgcag
                  |||
Sbjct:          1332 aattgaacatgaaacagggaccaagataacaatctcatctttgcag
hepatocellular carcinoma autoan> 300 I E H E T G T K I T I S S L Q

Query:          1026 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgt
                  |||
Sbjct:          1392 caaccggaaagaaccatcactgtgaagggcacagttgaggcctgt
hepatocellular carcinoma autoan> 320 N P E R T I T V K G T V E A C

Query:          1086 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctg
                  |||
Sbjct:          1452 agagattatgaagaagctgcgtgaggcctttgaaaatgatatgctg
hepatocellular carcinoma autoan> 340 E I M K K L R E A F E N D M L

Query:          1146 ctccggatacttctccagcctgtacccccatcaccagtttgcccg
                  |||
Sbjct:          1512 ctccggatacttctccagcctgtacccccatcaccagtttgcccg
hepatocellular carcinoma autoan> 360 S G Y F S S L Y P H H Q F G P

Query:          1206 ctcttatccagagcaggagattgtgaatctcttcatcccaaccag
                  |||
Sbjct:          1572 ctcttatccagagcaggagattgtgaatctcttcatcccaaccag
hepatocellular carcinoma autoan> 380 S Y P E Q E I V N L F I P T Q

Query:          1266 catcggaagaagggggcacacatcaaacagctggcgagattcgcc
                  |||
Sbjct:          1632 catcggaagaagggggcacacatcaaacagctggcgagattcgcc
hepatocellular carcinoma autoan> 400 I G K K G A H I K Q L A R F A

Query:          1326 gattgcccctgcggaaggcccagacgtcagcgaaaggatggtcac
                  |||
Sbjct:          1692 gattgcccctgcggaaggcccagacgtcagcgaaaggatggtcac
hepatocellular carcinoma autoan> 420 I A P A E G P D V S E R M V I

Query:          1386 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaa
                  |||
Sbjct:          1752 ggaagcccagttcaaggcccaggacggatctttgggaaactgaaa
hepatocellular carcinoma autoan> 440 E A Q F K A Q G R I F G K L K

Query:          1446 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcc
                  |||
Sbjct:          1812 taaccccaaagaagaagtgaagctggaagcgcatatcagagtgcc
hepatocellular carcinoma autoan> 460 N P K E E V K L E A H I R V P

Query:          1506 ccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaac
                  |||
Sbjct:          1872 ccgggtgattggcaaaggtggcaagaccgtgaacgaactgcagaac
```

```

hepatocellular carcinoma autoan> 480      R  V  I  G  K  G  G  K  T  V  N  E  L  Q  N

Query:                                     1566 agtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtg
                                          |||
Sbjct:                                     1932 agtcatcgtgcctcgtgaccaaacgccagatgaaaatgaggaagtg
hepatocellular carcinoma autoan> 500      V  I  V  P  R  D  Q  T  P  D  E  N  E  E  V

Query:                                     1626 cgggcacttcttttgctagccagactgcacagcgcaagatcagggaa
                                          |||
Sbjct:                                     1992 cgggcacttcttttgctagccagactgcacagcgcaagatcagggaa
hepatocellular carcinoma autoan> 520      G  H  F  F  A  S  Q  T  A  Q  R  K  I  R  E

Query:                                     1686 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgc
                                          |||
Sbjct:                                     2052 gaagcagcaggagcagaaataccctcagggagtcgcctcacagcgc
hepatocellular carcinoma autoan> 540      K  Q  Q  E  Q  K  Y  P  Q  G  V  A  S  Q  R

Query:                                     1746 ccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacac
                                          |||
Sbjct:                                     2112 ccacaggcaccagcaaaaacaacggatgaatgtagcccttccaacac

Query:                                     1806 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgag
                                          |||
Sbjct:                                     2172 ccaaacgcagccagccagatcgggagcaaaccaaagaccatctgag

Query:                                     1866 cggaggcgggccagggactctgccgaggccctgagaaccccaggggc
                                          |||
Sbjct:                                     2232 cggaggcgggccagggactctgccgaggccctgagaaccccaggggc

Query:                                     1926 gaaggtcagccagggtttgccagaaccaccgagccccgcctcccgcc
                                          |||
Sbjct:                                     2292 gaaggtcagccagggtttgccagaaccaccgagccccgcctcccgcc

Query:                                     1986 caggcttcagccatccacttcaccatccactcggatctctcctgaa
                                          |||
Sbjct:                                     2352 caggcttcagccatccacttcaccatccactcggatctctcctgaa

Query:                                     2046 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagc
                                          |||
Sbjct:                                     2412 tcccttttagttgaactaacataggtgaacgtgttcaaagccaagc

Query:                                     2106 ttttctgtggcaaatacgtctctgtacatgtgtgtacatattagaaa
                                          |||
Sbjct:                                     2472 ttttctgtgtggcaaatacgtctctgtacatgtgtgtacatattagaaa

Query:                                     2166 atatgtggcctgtgggttacacagggcgctgcagcggtaatatat
                                          |||
Sbjct:                                     2532 atatgtggcctgtgggttacacagggcgctgcagcggtaatatat

Query:                                     2226 atcaaataactcaactaactccaatttttaatcaattattaannnn
                                          |||
Sbjct:                                     2592 atcaaataactcaactaactccaatttttaatcaattattaatttt

```

Query: 2286 gagaaagcaggcttttctagactttaagaataaagtctttgggag  
|||||  
Sbjct: 2652 gagaaagcaggcttttctagactttaagaataaagtctttgggag

Query: 2346 agaggagctttgaggccaccgcacaaaattcacccagagggaaat  
|||||  
Sbjct: 2712 agaggagctttgaggccaccgcacaaaattcacccagagggaaat

Query: 2406 actcacggcagttctggatcacctgtgtatgtcaacagaagggata  
|||||  
Sbjct: 2772 actcacggcagttctggatcacctgtgtatgtcaacagaagggata

Query: 2466 aggaaactctgtcactcctcatgcctgtctagctcatacaccatt  
|||||  
Sbjct: 2832 aggaaactctgtcactcctcatgcctgtctagctcatacaccatt

Query: 2526 aggttttaactggttttttgcatactgctatataa 2561  
|||||  
Sbjct: 2892 aggttttaactggttttttgcatactgctatataa 2927

Score = 1035 bits (538), Expect = 0.0  
Identities = 608/665 (91%), Gaps = 2/665 (0%)  
Strand = Plus / Plus

Query: 2620 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcannnnnnnnnnn 2679  
|||||  
Sbjct: 2986 cattcttttgaatttcctcatccctccatctcaatcccgtatctacgcacccccccccc 3045

Query: 2680 nnaggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 2739  
|||||  
Sbjct: 3046 c-aggcaaagcagtgtctgtgagtatcacatcacacaaaaggaacaaaagcgaaacacaca 3104

Query: 2740 aaccagcctcaacttacacttgggttactcaaaagaacaagagtcaatggtacttgtccta 2799  
|||||  
Sbjct: 3105 aaccagcctcaacttacacttgggttactcaaaagaacaagagtcaatggtacttgtccta 3164

Query: 2800 gcgttttggagaggaaaacaggaacccaccaaaccaaatcaaccaaacaagaaaa 2859  
|||||  
Sbjct: 3165 gcgttttggagaggaaaacaggaacccaccaaaccaaatcaaccaaacaagaaaa 3224

Query: 2860 aattccacaatgaaagaatgtattttgcattttggtgtataagccatcaata 2919  
|||||  
Sbjct: 3225 aattccacaatgaaagaatgtattttgcattttggtgtataagccatcaata 3284

Query: 2920 ttcagcaaatgattcctttcttt-nnnnnnnnnntgtggaggaaagtagaaatttacc 2978  
|||||  
Sbjct: 3285 ttcagcaaatgattcctttcttttaaaaaaaaaaatgtggaggaaagtagaaatttacc 3344

Query: 2979 aaggttggtggccaggcggttaattcacagannnnnnnaacgagaaaaacacacagaa 3038  
|||||  
Sbjct: 3345 aaggttggtggccaggcggttaattcacagatttttttaacgagaaaaacacacagaa 3404



Query: 3039 gaagctacctcaggtgtttttacctcagcaccttgctcttggtgtttcccttagagatttt 3098  
|||||  
Sbjct: 3405 gaagctacctcaggtgtttttacctcagcaccttgatcttggtgtttcccttagagatttt 3464

Query: 3099 gtaaagctgatagttggagcannnnnnnnnnnnnaataaaaaatgagttggnnnnnnnn 3158  
|||||  
Sbjct: 3465 gtaaagctgatagttggagcatttttttatttttttaataaaaaatgagttggaaaaaaa 3524

Query: 3159 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3218  
|||||  
Sbjct: 3525 taagatatcaactgccagcctggagaaggtgacagtccaagtgtgcaacagctgttctga 3584

Query: 3219 attgtcttccgctagccaagaacnataatggccttcttttggacaaaccttgaaaatgtt 3278  
|||||  
Sbjct: 3585 attgtcttccgctagccaagaacctatatggccttcttttggacaaaccttgaaaatgtt 3644

Query: 3279 tattt 3283  
|||||  
Sbjct: 3645 tattt 3649

CPU time: 0.05 user secs. 0.00 sys. secs 0.05 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 13  
Number of Sequences: 0  
Number of extensions: 13  
Number of successful extensions: 8  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 2  
length of query: 3283  
length of database: 8,918,056,233  
effective HSP length: 26  
effective length of query: 3257  
effective length of database: 8,918,056,207  
effective search space: 29046109066199  
effective search space used: 29046109066199  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 22 (43.0 bits)



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

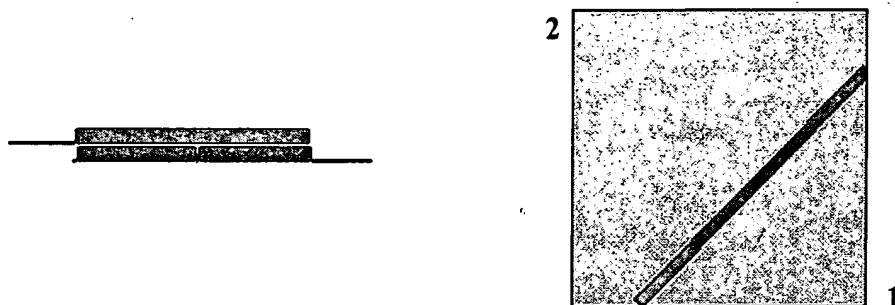
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq\_1 Length 577 (1..577)

Sequence 2 lcl|seq\_2 Length 1708 (1..1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0  
Identities = 438/445 (98%), Positives = 439/445 (98%)  
Frame = +2

```
Query: 133 RQAIMKLNQHLENHALKVSYPDEQITQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 192
          R AIMKLNQHLENHALKVSYPDEQI QGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 32  RGAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
          VDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 312
          CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI
Sbjct: 392 CSSACKMILEIMHKEAKDTKTADEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571

Query: 313 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAA 372
          SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA
Sbjct: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS --SHLIPGLNLAA 745

Query: 373 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 432
          VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS
Sbjct: 746 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 492
          RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI
Sbjct: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105

Query: 493 RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 552
          RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK
```

Sbjct: 1106RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKGQSNLAQARRK 577

IRDILAQVKQQHQKGQSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKGQSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

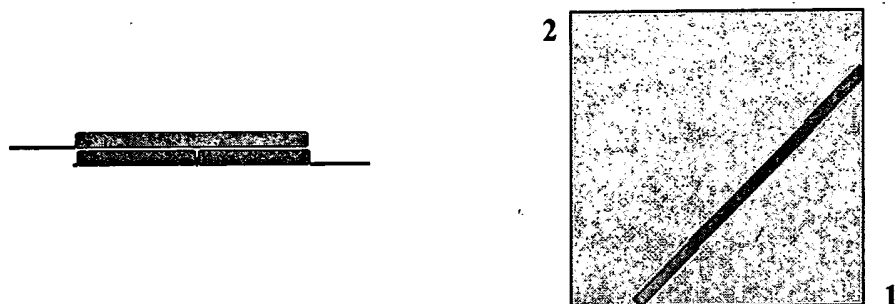
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq\_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq\_2 Length 1708 (1 .. 1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0  
 Identities = 438/445 (98%), Positives = 439/445 (98%)  
 Frame = +2

```

Query: 133 RQAIMKLNQHLENHALKVSYPDEQITQGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ 192
          R AIMKLNQHLENHALKVSYPDEQI QGPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 32  RQAIMKLNQHLENHALKVSYPDEQIAQQPENRRGGFGSRGQPRQGSPPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
          VDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 312
          CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI
Sbjct: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITI 571

Query: 313 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAA 372
          SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA
Sbjct: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAA 745

Query: 373 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 432
          VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS
Sbjct: 746 VGLFPASSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHI 492
          RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHI
Sbjct: 926 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKEENFFGPKKEEVKLETHI 1105

Query: 493 RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 552
          RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK
  
```

Sbjct: 1106RVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKGQSNLAQARRK 577

IRDILAQVKQQHQKGQSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKGQSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

●MIM

Taxonomy

Structure

c-myc-CRD

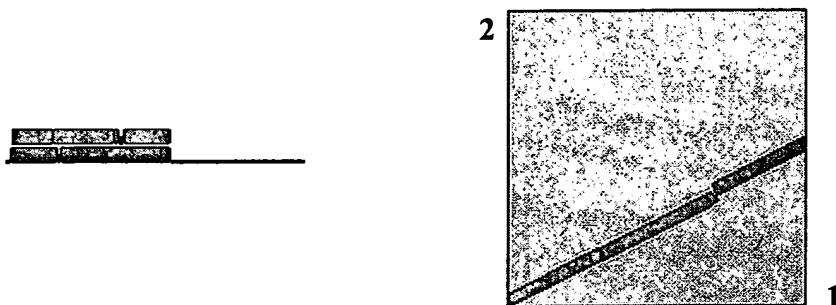
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq\_1 Length 577 (1..577)

Sequence 2 lcl|seq\_2 Length 3412 (1..3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0  
 Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)  
 Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFSGK 60
        MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61  VELQGRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSEETA 120
        VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVTYSNREQTRQAIMKLNQHLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178
        VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMKLSGHQFENYSFKISYIPDEEVSSPSPPPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
        A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENSG 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRN 298
        AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
        LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDLNPERTITVKGTVACASAEIEMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASSSAVPPP--PSSVTGAAPYSSFM----- 400
        + Q++LIPGLNL+A+G+F S + PP P AAPY F
  
```

Sbjct: 1138NQQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAAPYHPFTTHSGYFSSLYPHHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMV 454  
PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD RMV

Sbjct: 1318PPPHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMV 1497

Query: 455 VITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASAAGRVIGKGGKTVNELQ 514  
+ITGPPEAQFKAQGRI+GKLKEENFF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQ 1677

Query: 515 NLTAAEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQA 574  
NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NLTSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQVKQEQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

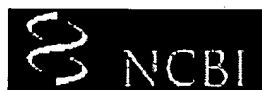
X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

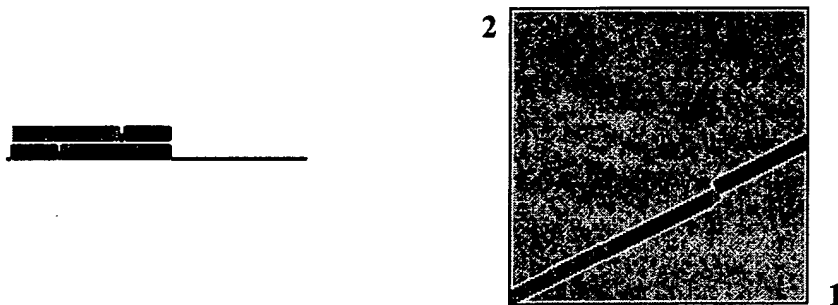
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq\_1 Length 577 (1..577)

Sequence 2 lcl|seq\_2 Length 3412 (1..3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0  
Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)  
Frame = +1

Query: 1 MNKLYIGNLNESVTPADLEKVF AEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60  
MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK  
Sbjct: 73 MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61 VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSEETA 120  
VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA  
Sbjct: 253 VELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121 VVNVTYSNREQTRQAIMKLNQHLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178  
VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q  
Sbjct: 433 VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179 QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238  
A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G  
Sbjct: 613 -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNTKQTQSRVDIHRKENS G 777

Query: 239 AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGLIGKEGRN 298  
AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRIGLIGKEGRN  
Sbjct: 778 AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHNGLVGRIGLIGKEGRN 957

Query: 299 LKKVEQDTEKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358  
LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+  
Sbjct: 958 LKKIEHETGKITISSLQDLSIYNPERTITVKGTVACASAEIEMKKLREAFENDMLAV 1137

Query: 359 SLQSHLIPGLNLAAVGLFPASSAVPPP--PSSVTGAAPYSSFM----- 400  
+ Q++LIPGLNL+A+G+F S + PP P AAPY F



Sbjct: 1138NQQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAAPYHPFTTHSGYFSSLYPHHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPD SKVRMV 454  
PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD RMV

Sbjct: 1318PFPHHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSE RMV 1497

Query: 455 VITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASAAGRVI GKGKTVNELQ 514  
+ITGPPEAQFKAQGRI+GKLKEENFF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQ 1677

Query: 515 NLTAAEVVPRDQTPDENQVIVKIIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQA 574  
NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NL TSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQVKQQEQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

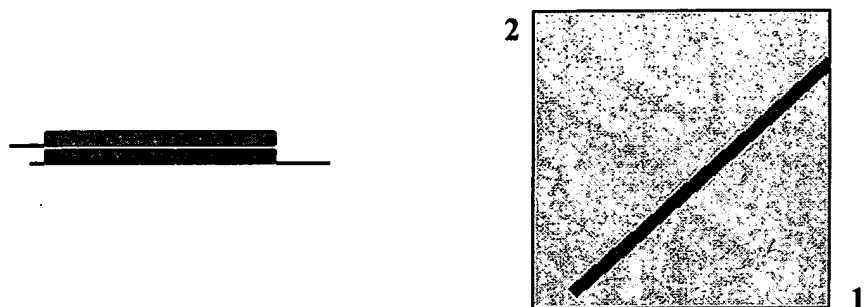
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq\_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq\_2 Length 1946 (1 .. 1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0  
Identities = 493/499 (98%), Positives = 494/499 (98%)  
Frame = +3

Query: 79 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 138  
RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK  
Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 287

Query: 139 LNGHQLENHALKVSYPDEQITQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQPVDIPL 198  
LNGHQLENHALKVSYPDEQI QGPENGRRGFGSRGQPRQGSPVAAGAPAKQQ VDIPL  
Sbjct: 288 LNGHQLENHALKVSYPDEQIAQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 258  
RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK  
Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 647

Query: 259 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 318  
MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL  
Sbjct: 648 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 827

Query: 319 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPA 378  
TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA  
Sbjct: 828 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS - -SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 438  
SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS  
Sbjct: 1002SSSAVPPPPSSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKKEENFFGPKKEEVKLETHIRVPASA 498  
IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGLKKEENFFGPKKEEVKLETHIRVPASA

Sbjct: 1182IKIAPPETPDSDKVRMVIITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 558  
AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQQHQKGQSNLAQARRK 577

QVKQQHQKGQSN AQARRK

Sbjct: 1542QVKQQHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

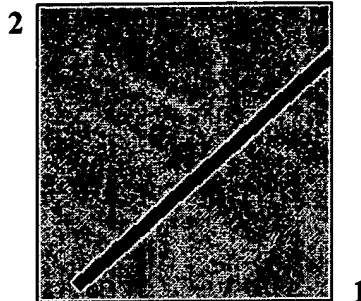
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** ☐ Filter ☐ Align

Sequence 1 lcl|seq\_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq\_2 Length 1946 (1 .. 1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0  
Identities = 493/499 (98%), Positives = 494/499 (98%)  
Frame = +3

Query: 79 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 138  
RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK  
Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTSESETAVVNVITYSNREQTRQAIMK 287

Query: 139 LNGHQLENHALKVSYPDEQITQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQPVDIPL 198  
LNGHQLENHALKVSYPDEQI QGPENGRRGFGSRGQPRQGSPVAAGAPAKQQ VDIPL  
Sbjct: 288 LNGHQLENHALKVSYPDEQIAQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK 258  
RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK  
Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSACK 647

Query: 259 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL 318  
MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL  
Sbjct: 648 MILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRNLKKVEQDTETKITISSLODL 827

Query: 319 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPA 378  
TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA  
Sbjct: 828 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 438  
SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS  
Sbjct: 1002SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA 498  
IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA

Sbjct: 1182IKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 558  
AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQOHQKGQSNLAQARRK 577  
QVKQOHQKGQSN AQARRK

Sbjct: 1542QVKQOHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

**c-myc-CRD**

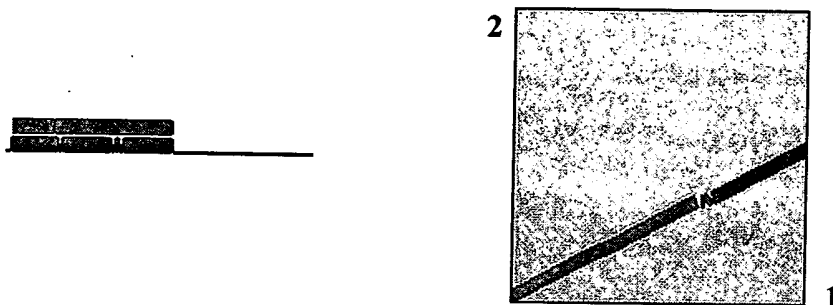
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq\_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq\_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0

Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)

Frame = +1

```
Query: 1  MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLS GK 252

Query: 61  VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSL LAQYGTVENCEQVNTESETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKKLSRKIQIRNIPHLQWEVL DGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVTYSNREQTRQAIMKLNHQLNHALKVSYIPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENS G 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGR LIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGR LIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAE EIPLKILAHNGLVGR LIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDL SIYNPERTITVKG TVEACASAEIEMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASS SAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 418
          + S G F SS P P+ PEQE+V +FIP QAVG
```

Sbjct: 1138NTHS-----GYF---SSLYPHHQFG-----PFPHHSYPEQEIVNLFIPTQAVG 1260  
Query: 419 AIIGKKGQHILSRFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEEN 478  
AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN  
Sbjct: 1261AIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIFGKLKEEN 1440  
Query: 479 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVPRDQTPDENQVIVK 538  
FF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQNLT+AEV+VPRDQTPDEN++VIV+  
Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNLTSAEVIVPRDQTPDENEEVIVR 1620  
Query: 539 IIGHFYASQMAQRKIRDILAQVKQQHQKQSNLAQARRK 577  
IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K  
Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQRSK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

Number of Sequences: 0

Number of extensions: 14230

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



# Blast 2 Sequences results

PubMed

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Structure

c-myc-CRD

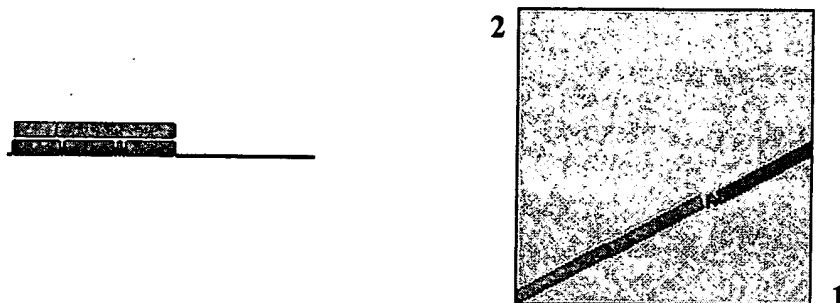
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lc|seq\_1 Length 577 (1 .. 577)

Sequence 2 lc|seq\_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0

Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)

Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFSGK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61  VELQGRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLAAQYGTVENCEQVNTESETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVITYSNREQTRQAIMKLNGHOLENHALKVSYIPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENSG 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRLLIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRLLIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEEIPLKILAHNGLVGRLLIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDLNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 418
          + S G F SS P P+ PEQE+V +FIP QAVG

```



Sbjct: 1138NTHS-----GYF---SSLYPHHQFG-----PFPHHHSYPEQEIVNLFIPTQAVG 1260  
Query: 419 AIIGKKKGQHIKQLSRFASASIKIAPPETPSKVRMVVITGPPEAQFKAQGRIYGKLKEEN 478  
AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN  
Sbjct: 1261AIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVITGPPEAQFKAQGRIFGKLKEEN 1440  
Query: 479 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAEEVVPRDQTPDENDQVIVK 538  
FF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQNLTAEV+VPRDQTPDEN++VIV+  
Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNLTAEVIVPRDQTPDENEEVIVR 1620  
Query: 539 IIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQARRK 577  
IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K  
Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQEQKYPQGVASQRSK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

Number of Sequences: 0

Number of extensions: 14230

Number of successful extensions: 17

Number of sequences better than 10.0: 2

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Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)